

SEQUENCE LISTING

<110> Rock, Charles O
Heath, Richard J

<120> Novel Enoyl Reductases and Methods of Use Thereof

<130> SJ-0022

<140> US 09/498,520

<141> 2000-02-04

<160> 62

<170> PatentIn version 3.1

<210> 1

<211> 975

<212> DNA

<213> Streptococcus pneumoniae

<400> 1

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atgggagcag gtgctctagc caaagcagtt gttcacggtg atgtggatgg tggctctggt      840
atggcaggtc aaatcgcagg gcttgtttct aaagaagaaa cagctgaaga aatcctaaaa      900
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<211> 324

<212> PRT

<213> Streptococcus pneumoniae

<400> 2

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Gln Gly Gly Met Ala Trp Val Ala Asp Gly Asp Leu Ala Gly Ala Val
 20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
 35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ser Leu Thr Asp Lys
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Val Glu Asp Ile
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
 85 90 95

Gly Asn Pro Ser Lys Tyr Met Glu Arg Phe His Glu Ala Gly Ile Ile
 100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
 115 120 125

Ile Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Ala Thr Ala
145 150 155 160

Ile Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly Glu Gly
 165 170 175

Ala Ala Ala Gly Phe Met Leu Gly Ala Glu Ala Val Gln Val Gly Thr
 180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Pro Asn Tyr Lys Glu
 195 200 205

Lys Ile Leu Lys Ala Arg Asp Ile Asp Thr Thr Ile Ser Ala Gln His
210 215 220

Phe Gly His Ala Val Arg Ala Ile Lys Asn Gln Leu Thr Arg Asp Phe
225 230 235 240

Glu Leu Ala Glu Lys Asp Ala Phe Lys Gln Glu Asp Pro Asp Leu Glu
 245 250 255

Ile Phe Glu Gln Met Gly Ala Gly Ala Leu Ala Lys Ala Val Val His
 260 265 270

Gly Asp Val Asp Gly Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu
 275 280 285

Val Ser Lys Glu Glu Thr Ala Glu Glu Ile Leu Lys Asp Leu Tyr Tyr
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Gly Ala Ala Lys Lys Ile Gln Glu Glu Ala Ser Arg Trp Thr Gly Val
 305 310 315 320

Val Arg Asn Asp

<210> 3
 <211> 966
 <212> DNA
 <213> Streptococcus mutans

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<211> 321

<212> PRT

<213> Streptococcus mutans

<400> 4

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Gln Gly Gly Met Ala Trp Val Ala Asp Gly Asp Leu Ala Gly Ala Val
20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ala Val Thr Asn Lys
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
85 90 95

Gly Asn Pro Gly Lys Tyr Ile Glu Arg Phe His Glu Ala Gly Ile Thr
100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Arg Arg Met Glu Lys
115 120 125

Leu Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Val Asp Ala
145 150 155 160

Val Asn Ile Pro Val Ile Gly Ala Gly Gly Val Ala Asp Gly Arg Gly
165 170 175

Ala Ala Ala Val Phe Met Leu Gly Ala Glu Ala Ile Gln Val Gly Thr
180 185 190

Arg Phe Ala Val Ala Lys Glu Ser Asn Ala His Ala Asn Phe Lys Lys
195 200 205

Lys Ile Leu Lys Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Ser Ile
210 215 220

Val Gly His Pro Val Arg Ala Ile Lys His Lys Leu Ser Ser Ala Tyr
225 230 235 240

Ala Thr Ala Glu Lys Glu Phe Leu Arg Gly Glu Lys Ser Gln Glu Asp
245 250 255

Ile Glu Val Leu Gly Ala Gly Ala Leu Arg Asn Ala Val Val Asp Gly
260 265 270

Asp Val Asp Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Phe Val
275 280 285

Thr Lys Glu Glu Thr Cys Glu Glu Ile Leu Lys Asp Leu Tyr Tyr Gly
290 295 300

Ala Ala Lys Val Ile Lys Ala Glu Ala Ala Arg Trp Ala Asp Val Glu
305 310 315 320

Lys

<210> 5
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<212> DNA
<213> Streptococcus pyogenes

<400> 5
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attactgata gaccttttgg ggtaaatatc atgcttttat ctctttttgc tgatgatatc 240
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aagtatatgg aaagactgca ccaggcgggt ataatcgttg ttcctgttgt cccaagcggt 360
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gctggaggac atattggcaa gttaacgact atgtcttttag taagacaagt tgttgaagcg 480
gtttcgattc ctgtcattgc ggcagggtgg atagctgatg gtcatggtgc agcagcagca 540
tttatggttag gagcagaggc tgttcaaatt ggaactcgct ttgttggtgc taaagaatcc 600

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gctaaagcag aaaaagcatt ttttaattggt caaaaaacag ctactgatat tgaagaaatg      780
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gctggccaaa ttgcagggct tgtgagaaaa gaagaaagct gtgaaacgat tttaaaagat      900
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<210> 6
<211> 323
<212> PRT
<213> Streptococcus pyogenes

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<400> 6

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Met Lys Thr Arg Ile Thr Glu Leu Leu Asn Ile Asp Tyr Pro Ile Phe
1           5           10           15

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Gln Gly Gly Met Ala Trp Val Ala Asp Gly Asp Leu Ala Gly Ala Val
          20           25           30

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Ser Asn Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
          35           40           45

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Glu Val Val Lys Ala Asn Ile Asp Arg Val Lys Ala Ile Thr Asp Arg
          50           55           60

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Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
65           70           75           80

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Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
          85           90           95

```

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Gly Asn Pro Gly Lys Tyr Met Glu Arg Leu His Gln Ala Gly Ile Ile
          100          105          110

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Val Val Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
          115          120          125

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Leu Gly Val Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
          130          135          140

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Ile Gly Lys Leu Thr Thr Met Ser Leu Val Arg Gln Val Val Glu Ala
145           150          155          160

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Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly His Gly
 165 170 175

Ala Ala Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Ile Gly Thr
 180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Gln Asn Phe Lys Asp
 195 200 205

Lys Ile Leu Ala Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Gln Val
 210 215 220

Val Gly His Pro Val Arg Ser Ile Lys Asn Lys Leu Thr Ser Ala Tyr
 225 230 235 240

Ala Lys Ala Glu Lys Ala Phe Leu Ile Gly Gln Lys Thr Ala Thr Asp
 245 250 255

Ile Glu Glu Met Gly Ala Gly Ser Leu Arg His Ala Val Ile Glu Gly
 260 265 270

Asp Val Val Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Val
 275 280 285

Arg Lys Glu Glu Ser Cys Glu Thr Ile Leu Lys Asp Ile Tyr Tyr Gly
 290 295 300

Ala Ala Arg Val Ile Gln Asn Glu Ala Lys Arg Trp Gln Ser Val Ser
 305 310 315 320

Ile Glu Lys

<210> 7

<211> 1068

<212> DNA

<213> Staphylococcus aureus COL

<400> 7

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ggcacaatag gcgcagggtta ctttaatacg cagcaattgg aagatgaaat agattatgta	180
cgccaattaa cgtcaaattc ttttggcgta aatgtctttg taccaagtca acaatcatat	240
accagtagtc aaattgaaaa tatgaatgca tgggttaaaac cttatcgacg cgcattacat	300

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ttagaagagc cggttgtaaa aattaccgaa gaacaacaat ttaagtgtca tattgatacg      360
ataattaaaa agcaagtgcc tgtatgttgt tttacttttg gaattccaag cgaacagatt      420
ataagcaggt tgaaagcagc gaatgtcaaa cttataggta cagcaacaag tgttgatgaa      480
gctattgcga atgaaaaagc gggtatggat gctatcggtg ctcaaggtag tgaagcaggt      540
ggacatcgtg gttcattttt aaaacctaaa aatcaattac ctatgggttg aacaatatct      600
ttagtgccac aaattgtaga tgtcgtttca attccgggtca ttgccgctgg tggaattatg      660
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caaatgagc taacaagtag cataagaaaa gccgcagcaa acatcggcga caaagagtta      960
atacatatgt ggagtggaca aagcccgcga ctagcaacaa cgcacccgc caacaccatc     1020
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<210> 8
<211> 355
<212> PRT
<213> Staphylococcus aureus COL
<400> 8

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Met Trp Asn Lys Asn Arg Leu Thr Gln Met Leu Ser Ile Glu Tyr Pro
1           5           10           15

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Ile Ile Gln Ala Gly Met Ala Gly Ser Thr Thr Pro Lys Leu Val Ala
          20           25           30

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Ser Val Ser Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
          35           40           45

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Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
          50           55           60

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Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
          65           70           75           80

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Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
          85           90           95

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Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
          100           105           110

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Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
340 345 350

Gln Tyr Lys
355

<210> 9
<211> 999
<212> DNA
<213> Enterococcus faecalis

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tcattagcaa gtgccgtgtc aaacgctggt ggattaggga ttattgctgg cggcaatgcc 180
ccaaaagaag tcgtaaaaaa agaaattaaa aaagttaaag aattaacgga gcaacccttt 240
gggtgtcaata ttatgttact ttcacctttt gccgatgaaa ttgtcgattt ggtttgtgaa 300
gaacagggttc ctgtcgtaac gacagggtgca ggcaatccag ccaaatacat ggctcgtttt 360
aaagaacata acattaaagt aatcccagta gttccttcag ttgcttttagc aaaaagaatg 420
gaaaaaattg gtgccgatgc tgtcattttt gaaggaatgg aagctgggtg acatattggc 480
aagttaacca ctatgagtgg cttaccgcaa atcgttgacg ctgtgtcaat tcctgtgatt 540
gcagcaggtg ggattgggtga tggctcggtg atggctgagg cctttatggt aggtgctgaa 600
gcagtcagtg taggcacacg ttttttaatt gccaaagaat gcaacgttca tccagattat 660
aaacagaaaag ttttaaaggc acgtgattta gatgcagtaa ttacctgtca acattttggc 720
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<210> 10
<211> 332
<212> PRT
<213> Enterococcus faecalis

<400> 10

Met Lys Cys Thr Tyr Leu Arg Thr Lys Gly Arg Ile Lys Ser Met Asn
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Gln Glu Leu Cys Glu Leu Leu Gly Ile Asn Tyr Pro Ile Phe Gln Gly
20 25 30

Gly Met Ala Trp Val Ala Asp Ala Ser Leu Ala Ser Ala Val Ser Asn
 35 40 45

Ala Gly Gly Leu Gly Ile Ile Ala Gly Gly Asn Ala Pro Lys Glu Val
 50 55 60

Val Lys Lys Glu Ile Lys Lys Val Lys Glu Leu Thr Glu Gln Pro Phe
 65 70 75 80

Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Glu Ile Val Asp
 85 90 95

Leu Val Cys Glu Glu Gln Val Pro Val Val Thr Thr Gly Ala Gly Asn
 100 105 110

Pro Ala Lys Tyr Met Ala Arg Phe Lys Glu His Asn Ile Lys Val Ile
 115 120 125

Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys Ile Gly
 130 135 140

Ala Asp Ala Val Ile Phe Glu Gly Met Glu Ala Gly Gly His Ile Gly
 145 150 155 160

Lys Leu Thr Thr Met Ser Gly Leu Pro Gln Ile Val Asp Ala Val Ser
 165 170 175

Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg Gly Met Ala
 180 185 190

Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Leu Gly Thr Arg Phe
 195 200 205

Leu Ile Ala Lys Glu Cys Asn Val His Pro Asp Tyr Lys Gln Lys Val
 210 215 220

Leu Lys Ala Arg Asp Leu Asp Ala Val Ile Thr Cys Gln His Phe Gly
 225 230 235 240

His Pro Val Arg Thr Leu Lys Asn Lys Leu Thr Ala Gln Tyr Asn Gln
 245 250 255

Leu Glu Lys Gln Glu Leu Gln Lys Glu Val Pro Asp Leu Glu Met Phe
 260 265 270

Glu Lys Ile Gly Gln Gly Ala Leu Arg Lys Ala Val Val Asp Gly Asp

275

280

285

Met Asp Tyr Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Lys
 290 295 300

Lys Glu Glu Thr Ala Gln Glu Ile Ile Asp Ser Leu Met Ser Glu Cys
 305 310 315 320

Lys Ala Ile Val His Lys Met Asn Gln Arg Trp Gly
 325 330

<210> 11
 <211> 933
 <212> DNA
 <213> Clostridium acetobutylicum

<400> 11
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 ataatagcag cagcaaatgc accagttgag tatgtaagag atgaaataag gaaggcaaaa 180
 aaacttacgg ataagccatt cggagttaat ataatgctct taagtgataa tgcagaagaa 240
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 gaagcagtag aagttataga tagaattaaa tag 933

<210> 12
 <211> 310
 <212> PRT
 <213> Clostridium acetobutylicum

<400> 12

Met Leu Lys Thr Gln Phe Cys Asp Ile Ile Gly Ile Lys Tyr Pro Ile
 1 5 10 15

Ile Gln Gly Gly Met Ala Trp Val Ala Asp Ser Ser Leu Ala Ala Gly
 20 25 30

Val Ser Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Ala Asn Ala Pro
 35 40 45

Val Glu Tyr Val Arg Asp Glu Ile Arg Lys Ala Lys Lys Leu Thr Asp
 50 55 60

Lys Pro Phe Gly Val Asn Ile Met Leu Leu Ser Asp Asn Ala Glu Glu
 65 70 75 80

Val Ala Lys Met Val Cys Glu Glu Gly Val Lys Val Val Thr Thr Gly
 85 90 95

Ala Gly Asn Pro Gly Lys Tyr Ile Asp Met Trp Lys Glu His Asp Ile
 100 105 110

Lys Val Ile Pro Val Val Ala Ser Val Ala Leu Ala Arg Arg Met Glu
 115 120 125

Arg Cys Gly Val Asp Ala Val Val Ala Glu Gly Cys Glu Ser Gly Gly
 130 135 140

His Val Gly Glu Leu Thr Thr Met Ala Leu Val Pro Gln Val Val Asp
 145 150 155 160

Ala Ile Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg
 165 170 175

Gly Val Ala Ala Ala Phe Ala Leu Gly Ala Ser Gly Val Gln Val Gly
 180 185 190

Thr Arg Phe Leu Ile Ala Lys Glu Cys Thr Val His Gln Asn Tyr Lys
 195 200 205

Asn Lys Val Leu Lys Ala Lys Asp Ile Asp Thr Glu Val Thr Gly Arg
 210 215 220

Ser Thr Gly His Pro Val Arg Val Leu Arg Asn Lys Leu Ala Arg Lys
 225 230 235 240

Tyr Lys Leu Met Glu Lys Glu Gly Ala Ser Pro Glu Glu Met Glu Glu

14

245

250

255

Leu Gly Arg Gly Ala Leu Pro Arg Ala Val Arg Glu Gly Asp Val Asp
260 265 270

Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Asn Lys Glu
275 280 285

Glu Thr Cys Asp Glu Ile Val Glu Ser Met Phe Lys Glu Ala Val Glu
290 295 300

Val Ile Asp Arg Ile Lys
305 310

<210> 13
<211> 930
<212> DNA
<213> Clostridium difficile

<400> 13
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acagataaac cttttggagt aaatgtaata cttatgtgcg catttggtga tgatataatt 240
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ttggcacaaa gaatggaaaa gctaggagct acagcagtaa tagcagaagg tactgaaggt 420
ggaggacata taggagaact tactactatg gtcttagttc cacaagttgc tgatgctgta 480
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gcattaggtg ccagtgcagt tcaagtagga actagattta ttgacagtga agagtgttct 600
gtccattcaa actataaaaa cttagtacta aaagcaaaag atagagatgc aattgtaaca 660
ggaagaagta ctggtcatcc agtaagaaca ttaaaaaata aactatcaa agaattttta 720
aagatgggaac aaaatggagc tactcctgaa gaattggata aaaaaggtag aggagcttta 780
agatttgcaa cagtagatgg agacatagaa aaagggtcat ttatggcagg tcaaagtgtc 840
gctatggtaa aagaaataac accttgtaag gaaattatag aggctatggt aaatcaagca 900
agagagatta tgccagcaat agaactgtaa 930

<210> 14
<211> 309
<212> PRT

<213> Clostridium difficile

<400> 14

Met Asn Lys Ile Cys Lys Ile Leu Asn Ile Lys Tyr Pro Val Ile Gln
 1 5 10 15

Gly Gly Met Ala Trp Val Ala Thr Ala Ser Leu Ala Ser Ala Val Ser
 20 25 30

Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Gly Asn Ala Pro Lys Glu
 35 40 45

Ala Ile Lys Lys Glu Ile Val Glu Cys Lys Lys Leu Thr Asp Lys Pro
 50 55 60

Phe Gly Val Asn Val Met Leu Met Ser Pro Phe Val Asp Asp Ile Ile
 65 70 75 80

Asp Leu Ile Ile Glu Glu Lys Val Gln Val Ile Thr Thr Gly Ala Gly
 85 90 95

Asn Pro Ala Lys Tyr Met Asp Arg Leu Lys Glu Ala Gly Thr Lys Val
 100 105 110

Ile Pro Val Val Pro Thr Ile Ala Leu Ala Gln Arg Met Glu Lys Leu
 115 120 125

Gly Ala Thr Ala Val Ile Ala Glu Gly Thr Glu Gly Gly Gly His Ile
 130 135 140

Gly Glu Leu Thr Thr Met Val Leu Val Pro Gln Val Ala Asp Ala Val
 145 150 155 160

Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Val Asp Gly Arg Gly Ile
 165 170 175

Ala Ala Ser Phe Ala Leu Gly Ala Ser Ala Val Gln Val Gly Thr Arg
 180 185 190

Phe Ile Cys Ser Glu Glu Cys Ser Val His Ser Asn Tyr Lys Asn Leu
 195 200 205

Val Leu Lys Ala Lys Asp Arg Asp Ala Ile Val Thr Gly Arg Ser Thr
 210 215 220

Gly His Pro Val Arg Thr Leu Lys Asn Lys Leu Ser Lys Glu Phe Leu

225 230 235 240
 Lys Met Glu Gln Asn Gly Ala Thr Pro Glu Glu Leu Asp Lys Lys Gly
 245 250 255
 Thr Gly Ala Leu Arg Phe Ala Thr Val Asp Gly Asp Ile Glu Lys Gly
 260 265 270
 Ser Phe Met Ala Gly Gln Ser Ala Ala Met Val Lys Glu Ile Thr Pro
 275 280 285
 Cys Lys Glu Ile Ile Glu Ala Met Val Asn Gln Ala Arg Glu Ile Met
 290 295 300
 Pro Ala Ile Glu Leu
 305

<210> 15
 <211> 873
 <212> DNA
 <213> Porphyromonas gingivalis W83

<400> 15
 atgaatagaa tttgcgaatt attgggtatc gaacatccga tcatatcggg aggcattggtg 60
 tgggtgcagcg gttggaaact ggcttctgct gtgagcaact gcggtggttt gggacttatt 120
 ggtgccggat ccatgcatcc ggacaatctg gagcatcaca tccgttcgtg taaagctgct 180
 acagacaagc ctttcggtgt gaacgtgcct cttctctatc cggagatgga caaaatcatg 240
 gagattatca tgaggggaaca tgtgcccgtg gtggtaacgt cagccggtag tccaaaggtg 300
 tggacagcca agttgaaagc tgccggtagc aagggtgatac atgtagttag cagtgccaca 360
 ttcgctcgca aatcagaggc agccggtgta gacgccatcg tggccgaagg gttcgaagcc 420
 ggcggacata atggacgaga ggagactacg accctctgtt tgatacctga agtagtggat 480
 gctgtgaaca ttcctgtggt tgctgccgga gggattgctt ccggccgtgc agttgccgct 540
 gctttggctt tgggtgccga tgccgtacaa gtggggaccc gttttgctct gagtaggaa 600
 agttcggcgc atgaagactt taaggcacat tgccgcgggt cgggtggagg agatacgatg 660
 ctttcgctca aggctgtatc gcctacgcga ctgctgaaga acaaattcta tcaggatgta 720
 ttcgctgccg agcagcgcgg tgcttccgtg gaagagctgc gcgagctgct cggtcgtggt 780
 cgtgccaaagc aaggtatttt cgaaggcgac ctgcacgagg gcgaattgga gataggccag 840
 gcagtatcgc agataagtca tgcggagacg gtg 873

<210> 16

<211> 313
 <212> PRT
 <213> Porphyromonas gingivalis W83

<400> 16

Met Asn Arg Ile Cys Glu Leu Leu Gly Ile Glu His Pro Ile Ile Ser
 1 5 10 15

Gly Gly Met Val Trp Cys Ser Gly Trp Lys Leu Ala Ser Ala Val Ser
 20 25 30

Asn Cys Gly Gly Leu Gly Leu Ile Gly Ala Gly Ser Met His Pro Asp
 35 40 45

Asn Leu Glu His His Ile Arg Ser Cys Lys Ala Ala Thr Asp Lys Pro
 50 55 60

Phe Gly Val Asn Val Pro Leu Leu Tyr Pro Glu Met Asp Lys Ile Met
 65 70 75 80

Glu Ile Ile Met Arg Glu His Val Pro Val Val Val Thr Ser Ala Gly
 85 90 95

Ser Pro Lys Val Trp Thr Ala Lys Leu Lys Ala Ala Gly Ser Lys Val
 100 105 110

Ile His Val Val Ser Ser Ala Thr Phe Ala Arg Lys Ser Glu Ala Ala
 115 120 125

Gly Val Asp Ala Ile Val Ala Glu Gly Phe Glu Ala Gly Gly His Asn
 130 135 140

Gly Arg Glu Glu Thr Thr Thr Leu Cys Leu Ile Pro Glu Val Val Asp
 145 150 155 160

Ala Val Asn Ile Pro Val Val Ala Ala Gly Gly Ile Ala Ser Gly Arg
 165 170 175

Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Asp Ala Val Gln Val Gly
 180 185 190

Thr Arg Phe Ala Leu Ser Glu Glu Ser Ser Ala His Glu Asp Phe Lys
 195 200 205

Ala His Cys Arg Arg Ser Val Glu Gly Asp Thr Met Leu Ser Leu Lys
 210 215 220

Ala Val Ser Pro Thr Arg Leu Leu Lys Asn Lys Phe Tyr Gln Asp Val
225 230 235 240

Phe Ala Ala Glu Gln Arg Gly Ala Ser Val Glu Glu Leu Arg Glu Leu
245 250 255

Leu Gly Arg Gly Arg Ala Lys Gln Gly Ile Phe Glu Gly Asp Leu His
260 265 270

Glu Gly Glu Leu Glu Ile Gly Gln Ala Val Ser Gln Ile Ser His Ala
275 280 285

Glu Thr Val Ala Glu Ile Met Val Asp Leu Val Asp Gly Tyr Lys Arg
290 295 300

Ser Leu Ala Gly Met Pro Thr Glu Ile
305 310

<210> 17
<211> 966
<212> DNA
<213> *Caulobacter crescentus*

<400> 17
atgggcctgc gcacgccgct gtgtgatctg ctggatatcg agcatccgat cctgctggcc 60
ggcatgggcg gggctctcta cgccccgctg gccgccgccg tctccaacgc cggcggctat 120
ggcgtcctgg gcatggccgg caccagcccg gacttcatcc gcgccagat gcgcgaggtc 180
aaaagcctga ccgacaagcc gttcgggggtg gacctgctgg ccgccacgcc ggatgcgctg 240
accgcgtccg tcgagggtcat catcgaggag ggcgcctcct catttgcgc gggcctgggc 300
gtgcccctgc cgatcatcga acgactcaag gccgccggcc tgaagggtcat ggtcgtctgc 360
ggagccgtga agcacgcggt caaggccgag caggcggggt gcgacgcggt gatctgcaa 420
ggcggcgagg gcggtggtca cacgggtctc gtcggcaccc tgccgctggt ggcccaggcc 480
gtggaggcgg tgaagatccc ggtggtcgcc gccggcggcc tgcattgacgg ccgcgggctg 540
gcggcgcccc tggctctggg cgcgcagggc gtctggatgg gcacgcggtt catgcctcg 600
cacgaggccc atgcgggcga tctctaccgc caggcgggtg tcgaggccgc cgacgaggac 660
acggtgcgca cgcgctgcta ctcgggcaag ccgatgcggg tgaagaagaa cccctatgtc 720
gacgactggg aagcgcgtcc cggcgacatc cagcccttcc cgcagcaggc catggtctcg 780
atccgcaatg gcgccatggg cggcatcggc ggccagatcg agggcctgga cgcggccaag 840
tcctgcttcg ccatgggcca gagcgccggc ggcgtgcgcg agatcttgcc ggccggcgag 900

atcgtcaagc ggctgatggc cgaggccgag acggcgctgg ccaaggcctc ggccttcagg 960

acctga 966

<210> 18

<211> 321

<212> PRT

<213> Caulobacter crescentus

<400> 18

Met Gly Leu Arg Thr Pro Leu Cys Asp Leu Leu Asp Ile Glu His Pro
1 5 10 15

Ile Leu Leu Ala Gly Met Gly Gly Val Ser Tyr Ala Pro Leu Ala Ala
20 25 30

Ala Val Ser Asn Ala Gly Gly Tyr Gly Val Leu Gly Met Ala Gly Thr
35 40 45

Ser Pro Asp Phe Ile Arg Ala Gln Met Arg Glu Val Lys Ser Leu Thr
50 55 60

Asp Lys Pro Phe Gly Val Asp Leu Leu Ala Ala Thr Pro Asp Ala Leu
65 70 75 80

Thr Ala Ser Val Glu Val Ile Ile Glu Glu Gly Ala Ser Ser Phe Val
85 90 95

Ala Gly Leu Gly Val Pro Leu Pro Ile Ile Glu Arg Leu Lys Ala Ala
100 105 110

Gly Leu Lys Val Met Val Val Cys Gly Ala Val Lys His Ala Val Lys
115 120 125

Ala Glu Gln Ala Gly Cys Asp Ala Val Ile Cys Gln Gly Gly Glu Gly
130 135 140

Gly Gly His Thr Gly Leu Val Gly Thr Leu Pro Leu Val Ala Gln Ala
145 150 155 160

Val Glu Ala Val Lys Ile Pro Val Val Ala Ala Gly Gly Leu His Asp
165 170 175

Gly Arg Gly Leu Ala Ala Ala Leu Ala Leu Gly Ala Gln Gly Val Trp
180 185 190

Met Gly Thr Arg Phe Ile Ala Ser His Glu Ala His Ala Gly Asp Leu

195

200

205

Tyr Arg Gln Ala Val Val Glu Ala Ala Asp Glu Asp Thr Val Arg Thr
 210 215 220

Arg Cys Tyr Ser Gly Lys Pro Met Arg Val Lys Lys Asn Pro Tyr Val
 225 230 235 240

Asp Asp Trp Glu Ala Arg Pro Gly Asp Ile Gln Pro Phe Pro Gln Gln
 245 250 255

Ala Met Val Ser Ile Arg Asn Gly Ala Met Gly Gly Ile Gly Gly Gln
 260 265 270

Ile Glu Gly Leu Asp Ala Ala Lys Ser Cys Phe Ala Met Gly Gln Ser
 275 280 285

Ala Gly Gly Val Arg Glu Ile Leu Pro Ala Gly Glu Ile Val Lys Arg
 290 295 300

Leu Met Ala Glu Ala Glu Thr Ala Leu Ala Lys Ala Ser Ala Phe Arg
 305 310 315 320

Thr

<210> 19
 <211> 987
 <212> DNA
 <213> Pseudomonas aeruginosa

<400> 19
 atgggctgtg tcaggacccg tttcaccgag accttcggcg tcgaacaccc gatcatgcag 60
 ggcggcatgc agtgggtcgg ccgtgccgag atggctgcgg cggaggccaa cgccgggtggc 120
 ctggcgacgc tgtcggcggtt gaccagccg agccggagg cactggctgc ggagattgcc 180
 cgctgccgag agctgaccga tcggccgttc ggggtcaacc tgaccttgcg gccgacgcag 240
 aagccgggtgc cctatgccga atatcgcgca gccatcatcg aggcgggaat ccgcgtcgtc 300
 gaaaccggcg gcaacgaccc cggcgagcac atcgccgaat tccgtcgaca cggcgtcaag 360
 gtgatccaca agtgaccgcg cgtgcgccat gcgctcaagg ccgagcgact gggcgtggac 420
 gccgtctcca tcgacggctt cgagtgtgcc ggccaccgag gcgaggacga catccccggc 480
 ctggtgttgc tgccggccgc ggccaaccgg ctacgcgtgc cgatcatcgc ctccggcggt 540
 ttcgccgatg gacgtggcct ggctcgggcg ctggcgctgg gtgccgacgc gatcaacatg 600

21

```

ggcacgcgct tcctggccac tcgcgaatgt ccgatacacc ctgcggtgaa ggcggcgatc 660
cgtgcgccgg acgagcggtc caccgacctg atcatgcggt ccctgcgcaa taccgcgccg 720
gtggcgcgca acgcgatcag ccaggaagta ctggcgatcg aggcacgcgg cggcgccggc 780
tacgccgata tcgccgcgct ggtcagcggc cagcgcggtc gccaggtgta ccagcagggc 840
gataccgacc tggggatctg gtcggccggc atgggtccagg gcctgatcga cgacgaaccg 900
gcctgcgccg agttgctcag ggacatcgtc gagcaggcgc gccaaactggt gcgtcaacgc 960
ctggagggca tgctcgccgg ggtctga 987

```

```

<210> 20
<211> 328
<212> PRT
<213> Pseudomonas aeruginosa

```

<400> 20

```

Met Gly Val Phe Arg Thr Arg Phe Thr Glu Thr Phe Gly Val Glu His
1           5           10          15

```

```

Pro Ile Met Gln Gly Gly Met Gln Trp Val Gly Arg Ala Glu Met Ala
20           25           30

```

```

Ala Ala Val Ala Asn Ala Gly Gly Leu Ala Thr Leu Ser Ala Leu Thr
35           40           45

```

```

Gln Pro Ser Pro Glu Ala Leu Ala Ala Glu Ile Ala Arg Cys Arg Glu
50           55           60

```

```

Leu Thr Asp Arg Pro Phe Gly Val Asn Leu Thr Leu Leu Pro Thr Gln
65           70           75           80

```

```

Lys Pro Val Pro Tyr Ala Glu Tyr Arg Ala Ala Ile Ile Glu Ala Gly
85           90           95

```

```

Ile Arg Val Val Glu Thr Ala Gly Asn Asp Pro Gly Glu His Ile Ala
100          105          110

```

```

Glu Phe Arg Arg His Gly Val Lys Val Ile His Lys Cys Thr Ala Val
115          120          125

```

```

Arg His Ala Leu Lys Ala Glu Arg Leu Gly Val Asp Ala Val Ser Ile
130          135          140

```

```

Asp Gly Phe Glu Cys Ala Gly His Pro Gly Glu Asp Asp Ile Pro Gly
145          150          155          160

```

Leu Val Leu Leu Pro Ala Ala Ala Asn Arg Leu Arg Val Pro Ile Ile
165 170 175

Ala Ser Gly Gly Phe Ala Asp Gly Arg Gly Leu Val Ala Ala Leu Ala
180 185 190

Leu Gly Ala Asp Ala Ile Asn Met Gly Thr Arg Phe Leu Ala Thr Arg
195 200 205

Glu Cys Pro Ile His Pro Ala Val Lys Ala Ala Ile Arg Ala Ala Asp
210 215 220

Glu Arg Ser Thr Asp Leu Ile Met Arg Ser Leu Arg Asn Thr Ala Arg
225 230 235 240

Val Ala Arg Asn Ala Ile Ser Gln Glu Val Leu Ala Ile Glu Ala Arg
245 250 255

Gly Gly Ala Gly Tyr Ala Asp Ile Ala Ala Leu Val Ser Gly Gln Arg
260 265 270

Gly Arg Gln Val Tyr Gln Gln Gly Asp Thr Asp Leu Gly Ile Trp Ser
275 280 285

Ala Gly Met Val Gln Gly Leu Ile Asp Asp Glu Pro Ala Cys Ala Glu
290 295 300

Leu Leu Arg Asp Ile Val Glu Gln Ala Arg Gln Leu Val Arg Gln Arg
305 310 315 320

Leu Glu Gly Met Leu Ala Gly Val
325

<210> 21

<211> 1044

<212> DNA

<213> Bacillus subtilis

<400> 21

atgaatgaat ttatgaaaaa gttttcttta acaaaaccga ttattcaagc tccaatggct 60
ggcgggtatta caaagcccg acttgcatct gcagtttcga atcaaggtgc tcttggcagc 120
ttagcatcgg ggtatcttac gccagacctc ctagaacaac aaataaaaaga aatatttgag 180
ctgacagacg ctctttttca aattaatgtg tttgttccgc taggtctaga gatgccacca 240
aaagatcaga ttaaaaagtg gaaagaaaac ataccgttag ctaatcaagt aaatcaattc 300

```

acatctgtac aagaagagtg ggatgacttc tatcaaaaaa ttgatctaata tttaaaatac 360
aagggttaagg cttgctcatt cacttttgat ctgccgcctg aagacgcagt aaaggagcta 420
aaaaccgctg gatgctgttt aataggaacc gcttcaacag tagaagaagc attgttaatg 480
gaagaacggg gaatggatat agtagtctt caaggaagtg aagccggtgg acatcgcgga 540
gcattcttac cttccaaagg tgaatctgcc gtaagggttaa tggctctgat tccacaagca 600
gcagatgcac tgagcgtacc tgtcatagct gctgggggaa tgatagacca cagaggagta 660
aaagcagctt taaccctcgg agcccaaggc gttcaaatac gttctgcctt ttttaattgt 720
cacgagagta acgcacatcc agtgcataaa cagaaaatac tagaagcaaa cgaagcagat 780
acaaagctta cgacattatt ttcaggtaaa gaggccagag gaatcgtaaa taaatggatg 840
gaagaaaatg aacagtttga gacacaaacc cttccgtacc cttatcaaaa tacactaacg 900
aaggcaatga gacagaaggc ttcacttcaa aataaccatg atcagatgtc tttatgggca 960
ggtcaaggga tacggtcatt gactgaggaa atttcgggta agcagctttt aaatcagctt 1020
tgccaagagg atataaaaat atag 1044

```

```

<210> 22
<211> 347
<212> PRT
<213> Bacillus subtilis

```

```

<400> 22

```

```

Met Asn Glu Phe Met Lys Lys Phe Ser Leu Thr Lys Pro Ile Ile Gln
1           5           10           15

```

```

Ala Pro Met Ala Gly Gly Ile Thr Lys Pro Arg Leu Ala Ser Ala Val
20           25           30

```

```

Ser Asn Gln Gly Ala Leu Gly Ser Leu Ala Ser Gly Tyr Leu Thr Pro
35           40           45

```

```

Asp Leu Leu Glu Gln Gln Ile Lys Glu Ile Phe Glu Leu Thr Asp Ala
50           55           60

```

```

Pro Phe Gln Ile Asn Val Phe Val Pro Leu Gly Leu Glu Met Pro Pro
65           70           75           80

```

```

Lys Asp Gln Ile Lys Lys Trp Lys Glu Asn Ile Pro Leu Ala Asn Gln
85           90           95

```

```

Val Asn Gln Phe Thr Ser Val Gln Glu Trp Asp Asp Phe Tyr Gln
100          105          110

```

Lys Ile Asp Leu Ile Leu Lys Tyr Lys Val Lys Ala Cys Ser Phe Thr
 115 120 125

Phe Asp Leu Pro Pro Glu Asp Ala Val Lys Glu Leu Lys Thr Ala Gly
 130 135 140

Cys Cys Leu Ile Gly Thr Ala Ser Thr Val Glu Glu Ala Leu Leu Met
 145 150 155 160

Glu Glu Arg Gly Met Asp Ile Val Val Leu Gln Gly Ser Glu Ala Gly
 165 170 175

Gly His Arg Gly Ala Phe Leu Pro Ser Lys Gly Glu Ser Ala Val Gly
 180 185 190

Leu Met Ala Leu Ile Pro Gln Ala Ala Asp Ala Leu Ser Val Pro Val
 195 200 205

Ile Ala Ala Gly Gly Met Ile Asp His Arg Gly Val Lys Ala Ala Leu
 210 215 220

Thr Leu Gly Ala Gln Gly Val Gln Ile Gly Ser Ala Phe Leu Ile Cys
 225 230 235 240

His Glu Ser Asn Ala His Pro Val His Lys Gln Lys Ile Leu Glu Ala
 245 250 255

Asn Glu Ala Asp Thr Lys Leu Thr Thr Leu Phe Ser Gly Lys Glu Ala
 260 265 270

Arg Gly Ile Val Asn Lys Trp Met Glu Glu Asn Glu Gln Phe Glu Thr
 275 280 285

Gln Thr Leu Pro Tyr Pro Tyr Gln Asn Thr Leu Thr Lys Ala Met Arg
 290 295 300

Gln Lys Ala Ser Leu Gln Asn Asn His Asp Gln Met Ser Leu Trp Ala
 305 310 315 320

Gly Gln Gly Ile Arg Ser Leu Thr Glu Glu Ile Ser Val Lys Gln Leu
 325 330 335

Leu Asn Gln Leu Cys Gln Glu Asp Ile Lys Ile
 340 345

<210> 23
 <211> 1128
 <212> DNA
 <213> Mycobacterium tuberculosis rv1533

<400> 23
 atgcggaacca gagtcgcca gctgctcggg gctgagtttc caatatgcgc gttcagccac 60
 tgccgggatg tgggtggcggc ggtgtccaat gcggtgcgggt tcgggatcct cggtgccgtc 120
 gcacatagcc ccaaaccggct ggagagcgag ctgacctgga tcgaggagca cacgggtggc 180
 aagccgtacg gagtcgacgt gctgctgccc cccaaatata tcggcgccga gcaaggcggg 240
 atcgatgccc agcaggcccc ggagctcata cccgaagggc atcgcacctt cgtcgacgac 300
 ttgctgggtc gctatggcat ccccgcggtc accgaccggc agcggttcgtc ctccggccgg 360
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 atccggttga tcgccagcgc gctcggggcc cgcaccagg atctcgtgga gcgcgcccac 480
 aaccatgacg tgctgggttc cgccctagcc ggacagcgcg agcacgcgcg gcgacacgcg 540
 gctgcgggtg ttgacctgat cgtcgcgagc ggcaccgagg ccggaggcca caccggcgag 600
 gtggcgacca tgggttctgg tcccgaagtc gtcgatgcgg tgcgccaac gccggtgctg 660
 gccgcggggc ggatcgcccc tggccgccag atcgctgcgg cgttgggcctt gggggcgga 720
 ggcgtctggt gcgggtcggg ctggttgacc accgaagaag ccgaaacgcc cccggtgggtc 780
 aaggacaagt ttctggccgc aacatcctcg gacacgggtg ggtcccggtc gctaaccggc 840
 aagccggcgc gcatgctgcg cacggcctgg accgacgaat gggatcgccc tgacagcccc 900
 gaccgccttg gcatgccgct gcagagcgcg ctggtcagcg accgcagtt gcgcatcaac 960
 caggccgcgc gccagcccgg ggccaaggct cgtgagctgg cgacctactt cgtcggacag 1020
 gtcgtcggtc cactcgaccg ggtgcggctc gcccgctcgg tgggtgcttga catggtcgag 1080
 gagttcatcg acaccgtcgg gcaactgcag ggggttggtc aaaggtga 1128

<210> 24
 <211> 375
 <212> PRT
 <213> Mycobacterium tuberculosis rv1533

<400> 24

Met Arg Thr Arg Val Ala Glu Leu Leu Gly Ala Glu Phe Pro Ile Cys
 1 5 10 15

Ala Phe Ser His Cys Arg Asp Val Val Ala Ala Val Ser Asn Ala Gly
 20 25 30

Gly Phe Gly Ile Leu Gly Ala Val Ala His Ser Pro Lys Arg Leu Glu

35

40

45

Ser Glu Leu Thr Trp Ile Glu Glu His Thr Gly Gly Lys Pro Tyr Gly
50 55 60

Val Asp Val Leu Leu Pro Pro Lys Tyr Ile Gly Ala Glu Gln Gly Gly
65 70 75 80

Ile Asp Ala Gln Gln Ala Arg Glu Leu Ile Pro Glu Gly His Arg Thr
85 90 95

Phe Val Asp Asp Leu Leu Val Arg Tyr Gly Ile Pro Ala Val Thr Asp
100 105 110

Arg Gln Arg Ser Ser Ser Ala Gly Gly Leu His Ile Ser Pro Lys Gly
115 120 125

Tyr Gln Pro Leu Leu Asp Val Ala Phe Ala His Asp Ile Arg Leu Ile
130 135 140

Ala Ser Ala Leu Gly Pro Pro Pro Pro Asp Leu Val Glu Arg Ala His
145 150 155 160

Asn His Asp Val Leu Val Ala Ala Leu Ala Gly Thr Ala Gln His Ala
165 170 175

Arg Arg His Ala Ala Ala Gly Val Asp Leu Ile Val Ala Gln Gly Thr
180 185 190

Glu Ala Gly Gly His Thr Gly Glu Val Ala Thr Met Val Leu Val Pro
195 200 205

Glu Val Val Asp Ala Val Ser Pro Thr Pro Val Leu Ala Ala Gly Gly
210 215 220

Ile Ala Arg Gly Arg Gln Ile Ala Ala Ala Leu Ala Leu Gly Ala Glu
225 230 235 240

Gly Val Trp Cys Gly Ser Val Trp Leu Thr Thr Glu Glu Ala Glu Thr
245 250 255

Pro Pro Val Val Lys Asp Lys Phe Leu Ala Ala Thr Ser Ser Asp Thr
260 265 270

Val Arg Ser Arg Ser Leu Thr Gly Lys Pro Ala Arg Met Leu Arg Thr
275 280 285

Ala Trp Thr Asp Glu Trp Asp Arg Pro Asp Ser Pro Asp Pro Leu Gly
 290 295 300

Met Pro Leu Gln Ser Ala Leu Val Ser Asp Pro Gln Leu Arg Ile Asn
 305 310 315 320

Gln Ala Ala Gly Gln Pro Gly Ala Lys Ala Arg Glu Leu Ala Thr Tyr
 325 330 335

Phe Val Gly Gln Val Val Gly Ser Leu Asp Arg Val Arg Ser Ala Arg
 340 345 350

Ser Val Val Leu Asp Met Val Glu Glu Phe Ile Asp Thr Val Gly Gln
 355 360 365

Leu Gln Gly Leu Val Gln Arg
 370 375

<210> 25
 <211> 1035
 <212> DNA
 <213> Mycobacterium tuberculosis rv2781c

<400> 25
 atggtgttgg gcttctggga catcgcggtg ccgatcgctg gcgccccgat ggccggcggc 60
 ccgagcacc cggcggttggc cgcggcggtg tccaacgctg gcgggcttgg ttctgctgcc 120
 ggcggctatc tgagcgcgga cgggctcgcc gacgatatcg ccgctgcgcg gcgccgcaact 180
 accggtccta tcggagccaa tctgtttgtg ccccaacca gcgtcgccga ctgggcgcag 240
 ctggagtatt acgcggacga gtcgaagag gtgcgcgagt actaccacac cgagggtgggc 300
 cagcccgctc atggtgacga cgacgactgg gtgcgcaaac tcgaggtggg agccgatggt 360
 cgtccggagg tgggtgctgt caccttcggc gcgccgccgc cggatgtcgt gcagcggttg 420
 agcgcgctgg gactgttggg ctcgatcacc gtgacgtcgg tctacgaggc cgggtgtggcc 480
 attgccgcgg gcgcggacag cctggtgggc cagggcccg cgcggcgcg gcaccgcgga 540
 acgttcgcgc cggacatgga acccggtacg gagtcgctgc accaactcct cgatcggatt 600
 ggcagcgccc atgatgtgcc gctggttgca gccgggtggc tgggcacggc tgaggacgtg 660
 gccgccgtgc tgcgcgcgg agcgatcgcc gcgcaggttg gtaccgcatt gctgctggcc 720
 gacgaagccg gtaccaatgc cgcacaccgt gccgcgctga agaatccaga gttcgatgcc 780
 accctgggtc ctcgggctgt ctcgggtagg tatgcgcgcg gtctggccaa caacttcact 840
 cgcctgctcg accacgtggc gccgctgggt tatccggagg tccaccagat gacgaagccg 900

atacgggagg cgagggtgca ggaggacgac ccgcacggaa caaacctttg ggagggatcg 960
 gcgcaccgga agaccgggcc ggagcccgcg gccgacatca tcgcttcct tactcccgac 1020
 gtgtgctcgg cgtaa 1035

<210> 26
 <211> 344
 <212> PRT
 <213> Mycobacterium tuberculosis rv2781c

<400> 26

Met Val Leu Gly Phe Trp Asp Ile Ala Val Pro Ile Val Gly Ala Pro
 1 5 10 15

Met Ala Gly Gly Pro Ser Thr Pro Ala Leu Ala Ala Val Ser Asn
 20 25 30

Ala Gly Gly Leu Gly Phe Val Ala Gly Gly Tyr Leu Ser Ala Asp Arg
 35 40 45

Leu Ala Asp Asp Ile Ala Ala Ala Arg Ala Ala Thr Thr Gly Pro Ile
 50 55 60

Gly Ala Asn Leu Phe Val Pro Gln Pro Ser Val Ala Asp Trp Ala Gln
 65 70 75 80

Leu Glu Tyr Tyr Ala Asp Glu Leu Glu Glu Val Ala Glu Tyr Tyr His
 85 90 95

Thr Glu Val Gly Gln Pro Val Tyr Gly Asp Asp Asp Asp Trp Val Arg
 100 105 110

Lys Leu Glu Val Val Ala Asp Val Arg Pro Glu Val Val Ser Phe Thr
 115 120 125

Phe Gly Ala Pro Pro Pro Asp Val Val Gln Arg Leu Ser Ala Leu Gly
 130 135 140

Leu Leu Val Ser Ile Thr Val Thr Ser Val Tyr Glu Ala Gly Val Ala
 145 150 155 160

Ile Ala Ala Gly Ala Asp Ser Leu Val Val Gln Gly Pro Ala Ala Gly
 165 170 175

Gly His Arg Gly Thr Phe Ala Pro Asp Met Glu Pro Gly Thr Glu Ser
 180 185 190

Leu His Gln Leu Leu Asp Arg Ile Gly Ser Ala His Asp Val Pro Leu
195 200 205

Val Ala Ala Gly Gly Leu Gly Thr Ala Glu Asp Val Ala Ala Val Leu
210 215 220

Arg Arg Gly Ala Ile Ala Ala Gln Val Gly Thr Ala Leu Leu Leu Ala
225 230 235 240

Asp Glu Ala Gly Thr Asn Ala Ala His Arg Ala Ala Leu Lys Asn Pro
245 250 255

Glu Phe Asp Ala Thr Leu Val Thr Arg Ala Phe Ser Gly Arg Tyr Ala
260 265 270

Arg Gly Leu Ala Asn Asn Phe Thr Arg Leu Leu Asp His Val Ala Pro
275 280 285

Leu Gly Tyr Pro Glu Val His Gln Met Thr Lys Pro Ile Arg Ala Ala
290 295 300

Ala Val Gln Ala Asp Asp Pro His Gly Thr Asn Leu Trp Ala Gly Ser
305 310 315 320

Ala His Arg Lys Thr Arg Pro Gly Pro Ala Ala Asp Ile Ile Ala Ser
325 330 335

Leu Thr Pro Asp Val Cys Ser Ala
340

<210> 27

<211> 1068

<212> DNA

<213> Mycobacterium tuberculosis rv3553

<400> 27

atgaggctgc gtacgccgct gaccgagctc atcggcatcg agcaccggt ggtgcagacc 60
gggatgggct ggggtggccgg tgcccggtcg gtgtcggcga ccgccaacgc gggcgggctg 120
ggcatcttgg cctcggccac catgacgctg gacgagctgg cggcggcgat cacaaaggtc 180
aaggcgtca ccgacaagcc attcggggtg aacatccgcg ccgacgcagc cgacgcgggc 240
gaccgcgtcg agttgatgat ccgcgagggg gtgcgggttg cctcggttcgc gttggcacc 300
aaacagcagc tgatcgcccg gctcaaagaa gccggcgcgg tggtcatacc gtcgatcggc 360
gcggccaaac atgcgcgcaa ggtggcgggc tggggcgccg acgcgatgat cgtgcagggc 420

```

ggcgagggcg gcggccacac cgggccggtc gccaccacgc tgctgttgcc gtcgggtgctg 480
gacgccgtgg cgggcaccgg catcccgtg atcgccgccc gcggcttctt cgacggggcg 540
gggctagccg cggcgttggt ctacggcgcc gccgggggtg ccatgggcac cgggtttctg 600
ctcacctcgg attccaccgt gcccgacgcg gtcaaacggc gttacctgca ggccggcttg 660
gacggcaccg tggtcaccac ccgcgtcgac gggatgccgc accgggtgct gcgcaccgag 720
ctggtcgaga agctggaaaag cggctcgcg gcacgaggtt tcgcggccgc gctgcgcaat 780
gccggcaagt ttagacggat gtcgcagatg acctggcggc cgatgatccg agacggcctg 840
accatgcgcc acggcaagga attgacctgg tcacaggtgc tgatggcggc aaacaccccg 900
atgctgctca aagccggcct ggtcgacggc aacaccgagg ccgggggtgct ggcatcgggc 960
caggtagcgg gcattcttga cgacctaccg tcgtgcaaag agctgatcga gtcgatcgtg 1020
cttgacgccca tcacacattt acaaaccgca tctgcgctgg tggagtga 1068

```

```

<210> 28
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis rv3553

```

```

<400> 28

```

```

Met Arg Leu Arg Thr Pro Leu Thr Glu Leu Ile Gly Ile Glu His Pro
1           5           10           15

```

```

Val Val Gln Thr Gly Met Gly Trp Val Ala Gly Ala Arg Leu Val Ser
          20           25           30

```

```

Ala Thr Ala Asn Ala Gly Gly Leu Gly Ile Leu Ala Ser Ala Thr Met
          35           40           45

```

```

Thr Leu Asp Glu Leu Ala Ala Ala Ile Thr Lys Val Lys Ala Val Thr
50           55           60

```

```

Asp Lys Pro Phe Gly Val Asn Ile Arg Ala Asp Ala Ala Asp Ala Gly
65           70           75           80

```

```

Asp Arg Val Glu Leu Met Ile Arg Glu Gly Val Arg Val Ala Ser Phe
          85           90           95

```

```

Ala Leu Ala Pro Lys Gln Gln Leu Ile Ala Arg Leu Lys Glu Ala Gly
100           105           110

```

```

Ala Val Val Ile Pro Ser Ile Gly Ala Ala Lys His Ala Arg Lys Val
115           120           125

```

Ala Ala Trp Gly Ala Asp Ala Met Ile Val Gln Gly Gly Glu Gly Gly
130 135 140

Gly His Thr Gly Pro Val Ala Thr Thr Leu Leu Leu Pro Ser Val Leu
145 150 155 160

Asp Ala Val Ala Gly Thr Gly Ile Pro Val Ile Ala Ala Gly Gly Phe
165 170 175

Phe Asp Gly Arg Gly Leu Ala Ala Ala Leu Cys Tyr Gly Ala Ala Gly
180 185 190

Val Ala Met Gly Thr Arg Phe Leu Leu Thr Ser Asp Ser Thr Val Pro
195 200 205

Asp Ala Val Lys Arg Arg Tyr Leu Gln Ala Gly Leu Asp Gly Thr Val
210 215 220

Val Thr Thr Arg Val Asp Gly Met Pro His Arg Val Leu Arg Thr Glu
225 230 235 240

Leu Val Glu Lys Leu Glu Ser Gly Ser Arg Ala Arg Gly Phe Ala Ala
245 250 255

Ala Leu Arg Asn Ala Gly Lys Phe Arg Arg Met Ser Gln Met Thr Trp
260 265 270

Arg Ser Met Ile Arg Asp Gly Leu Thr Met Arg His Gly Lys Glu Leu
275 280 285

Thr Trp Ser Gln Val Leu Met Ala Ala Asn Thr Pro Met Leu Leu Lys
290 295 300

Ala Gly Leu Val Asp Gly Asn Thr Glu Ala Gly Val Leu Ala Ser Gly
305 310 315 320

Gln Val Ala Gly Ile Leu Asp Asp Leu Pro Ser Cys Lys Glu Leu Ile
325 330 335

Glu Ser Ile Val Leu Asp Ala Ile Thr His Leu Gln Thr Ala Ser Ala
340 345 350

Leu Val Glu
355

<210> 29
 <211> 969
 <212> DNA
 <213> Mycobacterium tuberculosis rv0021c

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<400> 29
:  gtggtgctat cgacggcctt tagccagatg ttcggaatcg actatccgat agtgtccgcg      60
:
:  ccaatggact tgatcgccgg cggtgagctg gctgccgcgg taagtggcgc agggggactc      120
:
:  ggcctcatcg ggggcggcta tggggaccgg gattggttg cccggcagtt cgatctcgcc      180
:
:  gctggagcgc cgggtgggctg cgggttcac acctggtctt tggcccgcca accgcagctg      240
:
:  ctcgacctcg cgctgcagta tgagccggtg gcggtgatgc tgtcgttcgg ggaccccgcg      300
:
:  gttttcgctg acgccatcaa gtccgccgga acgcggttgg tctgccagat ccaaaaccgg      360
:
:  acccaggccg agcgagccct gcaggtcggc gccgatgtgt tggtaggtca gggcaccgag      420
:
:  gccggtgggc acggccacgg tccacgttcc accctgacct tggtagccga aatcgtcgac      480
:
:  ctggtcaccg cgcggggaac tgatatcccg gtgatcgccg ccggggggcat cgccgacggc      540
:
:  cggggccttg ccgccgcgtt gatgttgggc gccgccgggg tattggtcgg tacgcgcttc      600
:
:  tacgccacgg tcgaagcggt atccacaccg caggcgcggg acccgctgct ggcggccact      660
:
:  ggcgacgaca tgtgccgcac cactatctac gatcagctac ggcgctatcc ctggccgcaa      720
:
:  ggacacacga tgagcgtgct aagcaacgcc ctcaccgacc aattcgagga caccgaactc      780
:
:  gacattctcc atcgcaaga agccatggcc agatattggc gagccgttgc tgcgcgtgac      840
:
:  tacagcatcg ccaatgtcac cgccggtcaa gccgcggggc tggtagaatgc cgtcctgcca      900
:
:  gccgccgacg tgataaccgg tatggcgcaa caagcggcga ggacgctgac cgcgatgcgc      960
:
:  gccgtgtaa                                     969

```

<210> 30
 <211> 322
 <212> PRT
 <213> Mycobacterium tuberculosis rv0021c

<400> 30

```

Met Val Leu Ser Thr Ala Phe Ser Gln Met Phe Gly Ile Asp Tyr Pro
1           5           10           15

```

```

Ile Val Ser Ala Pro Met Asp Leu Ile Ala Gly Gly Glu Leu Ala Ala
20           25           30

```

```

Ala Val Ser Gly Ala Gly Gly Leu Gly Leu Ile Gly Gly Gly Tyr Gly
35           40           45

```


Asp Arg Asp Trp Leu Ala Arg Gln Phe Asp Leu Ala Ala Gly Ala Pro
50 55 60

Val Gly Cys Gly Phe Ile Thr Trp Ser Leu Ala Arg Gln Pro Gln Leu
65 70 75 80

Leu Asp Leu Ala Leu Gln Tyr Glu Pro Val Ala Val Met Leu Ser Phe
85 90 95

Gly Asp Pro Ala Val Phe Ala Asp Ala Ile Lys Ser Ala Gly Thr Arg
100 105 110

Leu Val Cys Gln Ile Gln Asn Arg Thr Gln Ala Glu Arg Ala Leu Gln
115 120 125

Val Gly Ala Asp Val Leu Val Ala Gln Gly Thr Glu Ala Gly Gly His
130 135 140

Gly His Gly Pro Arg Ser Thr Leu Thr Leu Val Pro Glu Ile Val Asp
145 150 155 160

Leu Val Thr Ala Arg Gly Thr Asp Ile Pro Val Ile Ala Ala Gly Gly
165 170 175

Ile Ala Asp Gly Arg Gly Leu Ala Ala Ala Leu Met Leu Gly Ala Ala
180 185 190

Gly Val Leu Val Gly Thr Arg Phe Tyr Ala Thr Val Glu Ala Leu Ser
195 200 205

Thr Pro Gln Ala Arg Asp Pro Leu Leu Ala Ala Thr Gly Asp Asp Met
210 215 220

Cys Arg Thr Thr Ile Tyr Asp Gln Leu Arg Arg Tyr Pro Trp Pro Gln
225 230 235 240

Gly His Thr Met Ser Val Leu Ser Asn Ala Leu Thr Asp Gln Phe Glu
245 250 255

Asp Thr Glu Leu Asp Ile Leu His Arg Glu Glu Ala Met Ala Arg Tyr
260 265 270

Trp Arg Ala Val Ala Ala Arg Asp Tyr Ser Ile Ala Asn Val Thr Ala
275 280 285

Gly Gln Ala Ala Gly Leu Val Asn Ala Val Leu Pro Ala Ala Asp Val

290

295

300

Ile Thr Gly Met Ala Gln Gln Ala Ala Arg Thr Leu Thr Ala Met Arg
 305 310 315 320

Ala Val

<210> 31
 <211> 1131
 <212> DNA
 <213> Mycobacterium tuberculosis rv1894c

<400> 31
 atgcacactg ccatttgcca cgagctcggt atcgagtttc ctatttttgc cttcactcac 60
 tgccgcgatg tgggtggcgc cgtcagcaaa gctgggtggtt ttggtgtgct cggagcagtt 120
 ggggttcacgc cggagcagct ggagatcgag ctcaactgga tcgatgaaca catcggcgac 180
 caccctacg gggtcgacat cgtgatcccg aacaagtacg agggcatgga ctcccagctg 240
 tcggcggatg agctcgccaa gacgctgcgg tcgatgggtcc cgcaggagca tctggacttc 300
 gcccgcaaga tcctcgccga tcatgggtgtc ccggtcgagg acgccgacga ggacagtctg 360
 cagctgctcg gttggaccga ggcgacggcc accccacagg tcgacgcggc gctgaagcac 420
 cccaagatga cgatggtcgc caacgcgctt ggcaccccc cagcggacat gatcaagcac 480
 atccacgact cgggtcgcaa ggtggccgca ttgtgcggt caccctcgca ggcccgcaag 540
 cagccgatg cgggcgtcga catcatcatc gccagggcg gcgaggccgg cgggcactgt 600
 ggcgaggtg gctccattgt gttgtggcct caggctgtca aggaggtagc gccggttccg 660
 gtgttggcgg cgggtggcat cggcagcggc cagcagatcg ctgcagcgtt ggcgctgggg 720
 acccaagggg catggaccgg ttgcagtggt ctgatggtcg aggaagccgc aaacaccgcg 780
 gttcaacagg ccgcatacgt caaggcgacc agccgcgaca ccgtgcgcag tcgttccttc 840
 acgggtaagc cggcccggat gctgcgcaac gactggactg aggcctggga gcaaccggag 900
 agcccgaagc cgctcggtat gccgttgcaa tacatgggtc ccggcatggc cgtcaaagcc 960
 acacataaat acccgaacga gaccgtcgac gtcgcgttca acccgggtgg gcaggttggt 1020
 gggcagttca ccaaggtgga aaagacggct accgttatcg aacgctgggt gcaggagtac 1080
 ctcgaggcga ccgcccgggt ggacgcactc aatgctgccg cgtccgtttg a 1131

<210> 32
 <211> 376
 <212> PRT
 <213> Mycobacterium tuberculosis rv1894c

<400> 32

Met His Thr Ala Ile Cys Asp Glu Leu Gly Ile Glu Phe Pro Ile Phe
1 5 10 15

Ala Phe Thr His Cys Arg Asp Val Val Val Ala Val Ser Lys Ala Gly
20 25 30

Gly Phe Gly Val Leu Gly Ala Val Gly Phe Thr Pro Glu Gln Leu Glu
35 40 45

Ile Glu Leu Asn Trp Ile Asp Glu His Ile Gly Asp His Pro Tyr Gly
50 55 60

Val Asp Ile Val Ile Pro Asn Lys Tyr Glu Gly Met Asp Ser Gln Leu
65 70 75 80

Ser Ala Asp Glu Leu Ala Lys Thr Leu Arg Ser Met Val Pro Gln Glu
85 90 95

His Leu Asp Phe Ala Arg Lys Ile Leu Ala Asp His Gly Val Pro Val
100 105 110

Glu Asp Ala Asp Glu Asp Ser Leu Gln Leu Leu Gly Trp Thr Glu Ala
115 120 125

Thr Ala Thr Pro Gln Val Asp Ala Ala Leu Lys His Pro Lys Met Thr
130 135 140

Met Val Ala Asn Ala Leu Gly Thr Pro Pro Ala Asp Met Ile Lys His
145 150 155 160

Ile His Asp Ser Gly Arg Lys Val Ala Ala Leu Cys Gly Ser Pro Ser
165 170 175

Gln Ala Arg Lys His Ala Asp Ala Gly Val Asp Ile Ile Ile Ala Gln
180 185 190

Gly Gly Glu Ala Gly Gly His Cys Gly Glu Val Gly Ser Ile Val Leu
195 200 205

Trp Pro Gln Val Val Lys Glu Val Ala Pro Val Pro Val Leu Ala Ala
210 215 220

Gly Gly Ile Gly Ser Gly Gln Gln Ile Ala Ala Ala Leu Ala Leu Gly
225 230 235 240

Thr Gln Gly Ala Trp Thr Gly Ser Gln Trp Leu Met Val Glu Glu Ala
245 250 255

Ala Asn Thr Ala Val Gln Gln Ala Ala Tyr Val Lys Ala Thr Ser Arg
260 265 270

Asp Thr Val Arg Ser Arg Ser Phe Thr Gly Lys Pro Ala Arg Met Leu
275 280 285

Arg Asn Asp Trp Thr Glu Ala Trp Glu Gln Pro Glu Ser Pro Lys Pro
290 295 300

Leu Gly Met Pro Leu Gln Tyr Met Val Ser Gly Met Ala Val Lys Ala
305 310 315 320

Thr His Lys Tyr Pro Asn Glu Thr Val Asp Val Ala Phe Asn Pro Val
325 330 335

Gly Gln Val Val Gly Gln Phe Thr Lys Val Glu Lys Thr Ala Thr Val
340 345 350

Ile Glu Arg Trp Val Gln Glu Tyr Leu Glu Ala Thr Ala Arg Leu Asp
355 360 365

Ala Leu Asn Ala Ala Ala Ser Val
370 375

<210> 33
<211> 945
<212> DNA
<213> Thermotoga maritima

<400> 33
atgaccgtga gaacaagagt gacagatctt ctggaaatag agcatccaat cctcatgggt 60
ggaatggcct gggcggaac tcccaccctc gcagcagcgg tatcggaggc gggaggactt 120
ggaatcatcg gatccggagc catgaagccg gacgacctga gaaaagcgat ctccgaactc 180
agacagaaga cggacaaacc cttcggtgta aacataatcc ttgtctctcc gtgggcggac 240
gatctcgtca aggtgtgcat agaagagaaa gtaccgctcg tcacgttcgg tgcgggaaac 300
ccaacgaagt acataaggga actcaaggaa aacggaacaa aggtgatacc cgttgtcgcc 360
tccgactctc tggcaaggat ggtggaaaga gcgggagcgg atgcggtgat agcgggaagg 420
atggagtccg gtggacacat aggtgaagtc acaaccttcg ttctcgtcaa caaagtctcc 480
aggagtgtga acatccccgt gatcgagcgg ggaggcatcg ccgacggaag aggtatggca 540

gccgccttcg cactcggagc ggaagccgtt cagatgggaa ccaggtttgt ggcgagtgtg 600
 gaaagcgacg tgcacccggt ttacaaagaa aagatcgatca aggccttccat aagagacacc 660
 gttgtgacgg gagccaaact tggacacccc gcgcgcgttc tcagaactcc ctttgcaagg 720
 aagatccagg agatggagtt tgaaaacccc atgcaggctg aagaaatgct ggtgggaagt 780
 ctcagaagag cggtcgttga aggcgatctg gagagaggat ccttcattgt gggacagagc 840
 gccggcttga tcgatgagat aaaaccggtg aagcagatca tagaggatat cctgaaggag 900
 ttcaaagaaa cgggtggagaa gctgaggggg tacatcgaag agtga 945

<210> 34
 <211> 314
 <212> PRT
 <213> Thermotoga maritima

<400> 34

Met Thr Val Arg Thr Arg Val Thr Asp Leu Leu Glu Ile Glu His Pro
1 5 10 15

Ile Leu Met Gly Gly Met Ala Trp Ala Gly Thr Pro Thr Leu Ala Ala
20 25 30

Ala Val Ser Glu Ala Gly Gly Leu Gly Ile Ile Gly Ser Gly Ala Met
35 40 45

Lys Pro Asp Asp Leu Arg Lys Ala Ile Ser Glu Leu Arg Gln Lys Thr
50 55 60

Asp Lys Pro Phe Gly Val Asn Ile Ile Leu Val Ser Pro Trp Ala Asp
65 70 75 80

Asp Leu Val Lys Val Cys Ile Glu Glu Lys Val Pro Val Val Thr Phe
85 90 95

Gly Ala Gly Asn Pro Thr Lys Tyr Ile Arg Glu Leu Lys Glu Asn Gly
100 105 110

Thr Lys Val Ile Pro Val Val Ala Ser Asp Ser Leu Ala Arg Met Val
115 120 125

Glu Arg Ala Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ser Gly
130 135 140

Gly His Ile Gly Glu Val Thr Thr Phe Val Leu Val Asn Lys Val Ser
145 150 155 160

Arg Ser Val Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly
165 170 175

Arg Gly Met Ala Ala Ala Phe Ala Leu Gly Ala Glu Ala Val Gln Met
180 185 190

Gly Thr Arg Phe Val Ala Ser Val Glu Ser Asp Val His Pro Val Tyr
195 200 205

Lys Glu Lys Ile Val Lys Ala Ser Ile Arg Asp Thr Val Val Thr Gly
210 215 220

Ala Lys Leu Gly His Pro Ala Arg Val Leu Arg Thr Pro Phe Ala Arg
225 230 235 240

Lys Ile Gln Glu Met Glu Phe Glu Asn Pro Met Gln Ala Glu Glu Met
245 250 255

Leu Val Gly Ser Leu Arg Arg Ala Val Val Glu Gly Asp Leu Glu Arg
260 265 270

Gly Ser Phe Met Val Gly Gln Ser Ala Gly Leu Ile Asp Glu Ile Lys
275 280 285

Pro Val Lys Gln Ile Ile Glu Asp Ile Leu Lys Glu Phe Lys Glu Thr
290 295 300

Val Glu Lys Leu Arg Gly Tyr Ile Glu Glu
305 310

<210> 35
<211> 1092
<212> DNA
<213> Helicobacter pylori

<400> 35
atggtatcaa cactcaaacc gctaaaaatc ggtaaacaca ccataaaatt ccctatTTTT 60
caaggggggca tgggtgtggg gattagctgg gatgaactag ctggaaatgt tgccaaagaa 120
ggggcctttag gagtgatttc agccgtaggg actggttatt ataaaaacat gcgttttgta 180
gaaaggattg tggctaaaaa accctttgaa gccttgaatt ttactccaa aaaagcgttg 240
aatgagattt ttgcaaacgc taggaaaatt tgcgggaaca agcctttggg ggccaatatt 300
ttatacgcta tcaatgacta tggccgtgtt ttaagggact cttgtgaggc gggggcgaa 360
attatcatta caggggctgg ttgcccact aacatgcctg aattcgctaa ggattttagc 420

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gatgtggcgc tcatccctat catttcctca gcgaaggctt taaaaatcct ttgtaaaaga 480
tggagcgatc gctataaaag aatcccggac gcattcattg tggaagggcc tttgagtggg 540
gggcatcagg gctttaaata cgaagattgt ttcaaagaag aattccaatt agaaaactta 600
gtgcctaaag tcgtggaagc ttctaaagaa tgggggaata tccctatcat cgccgcgggg 660
gggatttggg ataagaaaga tatagacacc atgttaagcc ttggagcgag tggggtgcaa 720
atggcgactc gtttttttagg cacgaaagaa tgcgacgcta aagcgtatgc cgatcttttg 780
cccacgctca aaaaagaaga tattttactc atcaaatcgc ctgtaggcta tccggctagg 840
gctatcaata cgggggtgat caaacgcatt gaagagggtg acgcgcctaa aatcgcatgc 900
gtgagcaatt gtgtagcgcc ttgtaacagg ggtgaagaag ctaaaaaggt gggctattgt 960
atcgctgatg gtttggggcg cagttattta ggaaacagag aagaggggct ttattttacc 1020
ggggctaatt gctatagagt ggataagatt atcagcgtgc atgaattgat taaagagctt 1080
acagagggtt aa 1092

```

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<210> 36
<211> 363
<212> PRT
<213> Helicobacter pylori

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<400> 36

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```

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
1           5           10           15

```

```

Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
          20           25           30

```

```

Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
          35           40           45

```

```

Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
          50           55           60

```

```

Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
65           70           75           80

```

```

Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu
          85           90           95

```

```

Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg
          100          105          110

```

```

Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu

```

115

120

125

Pro Thr Asn Met Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu
 130 135 140

Ile Pro Ile Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg
 145 150 155 160

Trp Ser Asp Arg Tyr Lys Arg Ile Pro Asp Ala Phe Ile Val Glu Gly
 165 170 175

Pro Leu Ser Gly Gly His Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys
 180 185 190

Glu Glu Phe Gln Leu Glu Asn Leu Val Pro Lys Val Val Glu Ala Ser
 195 200 205

Lys Glu Trp Gly Asn Ile Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp
 210 215 220

Lys Lys Asp Ile Asp Thr Met Leu Ser Leu Gly Ala Ser Gly Val Gln
 225 230 235 240

Met Ala Thr Arg Phe Leu Gly Thr Lys Glu Cys Asp Ala Lys Ala Tyr
 245 250 255

Ala Asp Leu Leu Pro Thr Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys
 260 265 270

Ser Pro Val Gly Tyr Pro Ala Arg Ala Ile Asn Thr Gly Val Ile Lys
 275 280 285

Arg Ile Glu Glu Gly Asn Ala Pro Lys Ile Ala Cys Val Ser Asn Cys
 290 295 300

Val Ala Pro Cys Asn Arg Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys
 305 310 315 320

Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly
 325 330 335

Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser
 340 345 350

Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly
 355 360

<210> 37
 <211> 825
 <212> DNA
 <213> Archaeoglobus fulgidus

<400> 37
 atgaacagga ttgctaaact cctcaaaacg aagtatccga tagttcaggg cccgatggcc 60
 ggaataactc tcggagaatt tgcttctaca gtgtctgagg ctggcgggct tggagttata 120
 gcttctgccg gcctttcgcc tgaaaaacta aaagaggaga tagagaaagt taagaacagg 180
 actgataagc ccttcgccgt gaacattcca atatatcagc cgggctcgga gaagaatctt 240
 gagactgcac ttaaagctga tgttgggatt atttacacct ctgcaggaag cccggagaaa 300
 tacactgaga gagtaaagga atccggggca aaagtcatac acaaggtgtc gaggttgaaa 360
 gaggggctga aagcggagaa ggcgggagtg gatgctgtgg ttgcgatggg ctttgaggcg 420
 ggagggatta tagggaggag tgggtgaaca tccttctgct tgattcctga gcttgccgac 480
 aacctcagca ttccagttgt agccgctggc gggatagcag atgagagggg atttgctgca 540
 gccctgattc tcggagcgga aggtgttgag attggcacga gactgcttgc aaccaaagag 600
 tgtcccgctgc cggaaagcat taagcaagct attttaaaag ccacctgcca ctccacgatg 660
 gttattgaga gcccggttgt aatgagagct ctcaagccag agctgagcgg agattctgag 720
 aatcctgctc tgggagggca ggtttcaggg ctgattaagg agattcttac ggttgaagag 780
 gtaatcagga aaattgcaga ggggctgaat aaagctaaat tctaa 825

<210> 38
 <211> 274
 <212> PRT
 <213> Archaeoglobus fulgidus

<400> 38

Met Asn Arg Ile Ala Lys Leu Leu Lys Thr Lys Tyr Pro Ile Val Gln
 1 5 10 15

Gly Pro Met Ala Gly Ile Thr Leu Gly Glu Phe Ala Ser Thr Val Ser
 20 25 30

Glu Ala Gly Gly Leu Gly Val Ile Ala Ser Ala Gly Leu Ser Pro Glu
 35 40 45

Lys Leu Lys Glu Glu Ile Glu Lys Val Lys Asn Arg Thr Asp Lys Pro
 50 55 60

Phe Ala Val Asn Ile Pro Ile Tyr Gln Pro Gly Ser Glu Lys Asn Leu

65		70		75		80
Glu Thr Ala Leu Lys Ala Asp Val Gly Ile Ile Tyr Thr Ser Ala Gly	85		90		95	
Ser Pro Glu Lys Tyr Thr Glu Arg Val Lys Glu Ser Gly Ala Lys Val	100		105		110	
Ile His Lys Val Ser Arg Leu Lys Glu Gly Leu Lys Ala Glu Lys Ala	115		120		125	
Gly Val Asp Ala Val Val Ala Met Gly Phe Glu Ala Gly Gly Ile Ile	130		135		140	
Gly Arg Ser Gly Val Thr Ser Phe Cys Leu Ile Pro Glu Leu Ala Asp	145		150		155	160
Asn Leu Ser Ile Pro Val Val Ala Ala Gly Gly Ile Ala Asp Glu Arg	165		170		175	
Gly Phe Ala Ala Ala Leu Ile Leu Gly Ala Glu Gly Val Glu Ile Gly	180		185		190	
Thr Arg Leu Leu Ala Thr Lys Glu Cys Pro Val Pro Glu Ser Ile Lys	195		200		205	
Gln Ala Ile Leu Lys Ala Thr Cys Asp Ser Thr Met Val Ile Glu Ser	210		215		220	
Pro Val Val Met Arg Ala Leu Lys Pro Glu Leu Ser Gly Asp Ser Glu	225		230		235	240
Asn Pro Ala Leu Gly Gly Gln Val Ser Gly Leu Ile Lys Glu Ile Leu	245		250		255	
Thr Val Glu Glu Val Ile Arg Lys Ile Ala Glu Gly Leu Asn Lys Ala	260		265		270	

Lys Phe

<210> 39
 <211> 1125
 <212> DNA
 <213> Williopsis saturnus
 <400> 39

```

atgagatcac aaatacagag cttcctaaag acgtttgaag tcaggtatcc tattattcag      60
gccccaatgg ctggcgcttc gaccttgga ctcgcagcca ccgtaaccag actcggaggc      120
attgggttcga tccctatggg ctgctgagt gagaagtgtg atgctattga gacccagctg      180
gaaaattttg atgaattggg tggtgattct ggaaggatag tcaacttgaa cttctttgct      240
cataaggagc ctggttctgg gagagctgat gtcaacgagg aatgggtcaa gaagtatgac      300
aagatatatg gcaaagccgg aattgagttt gacaaaaagg agctgaagtt gttatatcca      360
tcttttaggt ccattgttga tccacaacat ccgactgtgc ggctactgaa gaatctcaag      420
ccaaagattg tcagtttcca ctttgggtta ccccatgagg cggtgattga atctctccag      480
gcaagcgata ttaagatctt tgtcactgtc acaaatctac aggagtttca gcaggcttat      540
gagtctaaat tggatgggtg cgtcctacaa ggatgggaag ctggtggaca tcgtggtaat      600
ttcaaggcta atgacgtcga agatgggaaa ctgaagacgt tggatctcgt tagtactatt      660
gttgattaca ttgactcggc tagtatctcc aatccaccat ttatcattgc agcgggtggt      720
attcatgatg atgagtccat caaagaattg cttcaattca acattgctgc cgttcagttg      780
ggtaactgtt ggttaccatc gagccaggcc acaatatctc ctgaacattt gaagatgttt      840
caatccccaa aaagtgcac gatgatgacc gcagccattt caggacgtaa cttgagaacg      900
atcagtacac ctttcttgag ggatcttcat caatcttcac cattggcctc gatccctgat      960
tatccattac cttacgacag ctttaagtca cttgctaata acgctaagca aagtggaaaa     1020
gggcctcagt actccgcatt tcttgctgga tctaactatc acaaatcttg gaaggatacg     1080
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<210> 40
<211> 374
<212> PRT
<213> Williopsis saturnus

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<400> 40
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Met Arg Ser Gln Ile Gln Ser Phe Leu Lys Thr Phe Glu Val Arg Tyr
1           5           10          15

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Pro Ile Ile Gln Ala Pro Met Ala Gly Ala Ser Thr Leu Glu Leu Ala
          20          25          30

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Ala Thr Val Thr Arg Leu Gly Gly Ile Gly Ser Ile Pro Met Gly Ser
          35          40          45

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Leu Ser Glu Lys Cys Asp Ala Ile Glu Thr Gln Leu Glu Asn Phe Asp
          50          55          60

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Glu Leu Val Gly Asp Ser Gly Arg Ile Val Asn Leu Asn Phe Phe Ala
65 70 75 80

His Lys Glu Pro Arg Ser Gly Arg Ala Asp Val Asn Glu Glu Trp Leu
85 90 95

Lys Lys Tyr Asp Lys Ile Tyr Gly Lys Ala Gly Ile Glu Phe Asp Lys
100 105 110

Lys Glu Leu Lys Leu Leu Tyr Pro Ser Phe Arg Ser Ile Val Asp Pro
115 120 125

Gln His Pro Thr Val Arg Leu Leu Lys Asn Leu Lys Pro Lys Ile Val
130 135 140

Ser Phe His Phe Gly Leu Pro His Glu Ala Val Ile Glu Ser Leu Gln
145 150 155 160

Ala Ser Asp Ile Lys Ile Phe Val Thr Val Thr Asn Leu Gln Glu Phe
165 170 175

Gln Gln Ala Tyr Glu Ser Lys Leu Asp Gly Val Val Leu Gln Gly Trp
180 185 190

Glu Ala Gly Gly His Arg Gly Asn Phe Lys Ala Asn Asp Val Glu Asp
195 200 205

Gly Gln Leu Lys Thr Leu Asp Leu Val Ser Thr Ile Val Asp Tyr Ile
210 215 220

Asp Ser Ala Ser Ile Ser Asn Pro Pro Phe Ile Ile Ala Ala Gly Gly
225 230 235 240

Ile His Asp Asp Glu Ser Ile Lys Glu Leu Leu Gln Phe Asn Ile Ala
245 250 255

Ala Val Gln Leu Gly Thr Val Trp Leu Pro Ser Ser Gln Ala Thr Ile
260 265 270

Ser Pro Glu His Leu Lys Met Phe Gln Ser Pro Lys Ser Asp Thr Met
275 280 285

Met Thr Ala Ala Ile Ser Gly Arg Asn Leu Arg Thr Ile Ser Thr Pro
290 295 300

Phe Leu Arg Asp Leu His Gln Ser Ser Pro Leu Ala Ser Ile Pro Asp
305 310 315 320

Tyr Pro Leu Pro Tyr Asp Ser Phe Lys Ser Leu Ala Asn Asp Ala Lys
325 330 335

Gln Ser Gly Lys Gly Pro Gln Tyr Ser Ala Phe Leu Ala Gly Ser Asn
340 345 350

Tyr His Lys Ser Trp Lys Asp Thr Arg Ser Thr Glu Glu Ile Phe Ser
355 360 365

Ile Leu Val Gln Asp Leu
370

<210> 41
<211> 1215
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 41
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cctatggcgg gggtcacgac tattgaaatg gccgctaagg cttgtattgc gggcgccata 180
gcttcactac ccctatccca cttagacttc agaaagggtca atgatattga aaagcttaaa 240
ctgatgggtt cacaattcag agatcaagta gccgatgaat ctttagaggg caatctcaac 300
ctaaactttt ttgccatga tatcgttgat aaaccgaccg atcttcaaac agctaactgg 360
gcgaagctat acagaaagtc tatgaatgtg ccgattgata tgaatgagat taaattcgat 420
aatggtaatg tatcttttaa ggcatgtgaa aaagaaaatg ctcttcaaga ttttttccag 480
tacctatcag atggcttttag gcctaaaatc attagtttcc attttggcca tccgtcgaaa 540
tctacaatag aatatttaca aaaaattgga attctaattt ttgtgactgc cacctctgta 600
agagaagttc gattgttagc acgtctcggc attaattggc tagtgtgtca aggctatgaa 660
gcgaggaggac atagaggaaa tttcttagta aatgaccca aagatgatga aaacttatca 720
actgtacaat tggtgaaaag aacagttgat gaacttgctg aaatgaaaaa taaagggtctt 780
atacatgcta ctccctttgt cattgcagca ggtgggtataa tggattcaa agatatatca 840
tacatgttat cacagcaagc agacgtgtgt caagtgggga ctgcttttct tggttgcagt 900
gaatccaatg catcaaaaaa cttttcaagc cccttcactc gagaaacaac aactaaaatg 960
gttaatataa tatcaggaaa gcctgcaagg accatctcta ctctttttat cgaaaaagtc 1020
attgctaatt ttcaagggtga ggagcttctt ccatatgggt acatgtatag tgctttcaag 1080

caagtaagaa aaaagtatcc agaattggct aactttattt tagctggaca aggatttcag 1140
aatgtccaat caggaatcac aacagacaag aaaattgaaa ctatgggcgc aagattgaaa 1200
attgtcgga aataa 1215

<210> 42
<211> 404
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 42

Met Tyr Phe Leu Asn Gln Leu Ile Phe Gln Asp Val Ser Val Met Ser
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Val Asp Lys Arg Glu Asp Met Ser Arg Ser Phe Gln Lys Cys Leu Asn
20 25 30

Leu Arg Tyr Pro Ile Ile Gln Ala Pro Met Ala Gly Val Thr Thr Ile
35 40 45

Glu Met Ala Ala Lys Ala Cys Ile Ala Gly Ala Ile Ala Ser Leu Pro
50 55 60

Leu Ser His Leu Asp Phe Arg Lys Val Asn Asp Ile Glu Lys Leu Lys
65 70 75 80

Leu Met Val Ser Gln Phe Arg Asp Gln Val Ala Asp Glu Ser Leu Glu
85 90 95

Gly Asn Leu Asn Leu Asn Phe Phe Cys His Asp Ile Val Asp Lys Pro
100 105 110

Thr Asp Leu Gln Thr Ala Asn Trp Ala Lys Leu Tyr Arg Lys Ser Met
115 120 125

Asn Val Pro Ile Asp Met Asn Glu Ile Lys Phe Asp Asn Gly Asn Val
130 135 140

Ser Phe Lys Ala Phe Glu Lys Glu Asn Ala Leu Gln Asp Phe Phe Gln
145 150 155 160

Tyr Leu Ser Asp Gly Phe Arg Pro Lys Ile Ile Ser Phe His Phe Gly
165 170 175

His Pro Ser Lys Ser Thr Ile Glu Tyr Leu Gln Lys Ile Gly Ile Leu
180 185 190

Ile Phe Val Thr Ala Thr Ser Val Arg Glu Val Arg Leu Leu Ala Arg
 195 200 205

Leu Gly Ile Asn Gly Ile Val Cys Gln Gly Tyr Glu Ala Gly Gly His
 210 215 220

Arg Gly Asn Phe Leu Val Asn Asp Pro Lys Asp Asp Glu Asn Leu Ser
 225 230 235 240

Thr Val Gln Leu Val Lys Arg Thr Val Asp Glu Leu Ala Glu Met Lys
 245 250 255

Asn Lys Gly Leu Ile His Ala Thr Pro Phe Val Ile Ala Ala Gly Gly
 260 265 270

Ile Met Asp Ser Lys Asp Ile Ser Tyr Met Leu Ser Gln Gln Ala Asp
 275 280 285

Ala Val Gln Val Gly Thr Ala Phe Leu Gly Cys Ser Glu Ser Asn Ala
 290 295 300

Ser Lys Asn Phe Ser Ser Pro Phe Thr Arg Glu Thr Thr Thr Lys Met
 305 310 315 320

Val Asn Ile Ile Ser Gly Lys Pro Ala Arg Thr Ile Ser Thr Pro Phe
 325 330 335

Ile Glu Lys Val Ile Ala Asn Phe Gln Gly Glu Glu Leu Pro Pro Tyr
 340 345 350

Gly Tyr Met Tyr Ser Ala Phe Lys Gln Val Arg Lys Lys Tyr Pro Glu
 355 360 365

Leu Ala Asn Phe Ile Leu Ala Gly Gln Gly Phe Gln Asn Val Gln Ser
 370 375 380

Gly Ile Thr Thr Asp Lys Lys Ile Glu Thr Met Gly Ala Arg Leu Lys
 385 390 395 400

Ile Val Gly Lys

<210> 43
 <211> 1137
 <212> DNA

<213> *Neurospora crassa*

<400> 43

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atcgccaacg gcaactcttg gcgccgaggt tccaaggccg gcggtattgg ctttgtcgcc      180
ggcgggtccg acttcgccc cggtcctcc cacctaaccg cctctctac cgaactcgcc      240
tccgcccga gccgcctcgg tcttaccgac cgcacctca cccctctccc cggtattggc      300
gtcggcctca ttttaaccca caccatctcc gttccctacg taaccgacac cgtcctgccc      360
atcctgatcg aacactcccc gcaagcagtc tggctcttcg ccaacgaccc ggatttcgag      420
gcctcttcgg agcctggcgc aaagggaaca gcaaagcaaa tcatcgaggc ccttcacgct      480
tcgggggtcg tgggtattctt tcaagtaggc acggtgaaag atgcaaggaa ggcggcggca      540
gatggggcag atgtgattgt tgcgcaaggg atcgatgcgg gagggcatca gcttgctaca      600
gggagtggga ttgtgagttt ggtaccggag gttaggata tgcttgatag agagttcaag      660
gaacgagagg tgggtggtgt ggcggcggga ggtgtggcgg atgggagggg ggttgtaggg      720
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gacgggagag ccgttcgcaa tgcctcctac gacgaccacg cggccggtgt cccctttgaa      960
gagaatcaca agaagttcaa ggaggcagcg agctctgggg ataactcgcg ggctgtgact     1020
tggtccggga ctgctgtggg tctgataaag gaccagaggg cggctggcga tattgttagg     1080
gagttgaggg aagaggccaa agagaggatc aagaagattc aggccttttc tgcttaa      1137

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<210> 44

<211> 378

<212> PRT

<213> *Neurospora crassa*

<400> 44

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Met His Phe Pro Gly His Ser Ser Lys Lys Glu Glu Ser Ala Gln Ala
1          5          10          15

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Ala Leu Thr Lys Leu Asn Ser Trp Phe Pro Thr Thr Lys Asn Pro Val
          20          25          30

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Ile Ile Ser Ala Pro Met Tyr Leu Ile Ala Asn Gly Thr Leu Ala Ala
          35          40          45

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Glu Val Ser Lys Ala Gly Gly Ile Gly Phe Val Ala Gly Gly Ser Asp
 50 55 60

Phe Arg Pro Gly Ser Ser His Leu Thr Ala Leu Ser Thr Glu Leu Ala
 65 70 75 80

Ser Ala Arg Ser Arg Leu Gly Leu Thr Asp Arg Pro Leu Thr Pro Leu
 85 90 95

Pro Gly Ile Gly Val Gly Leu Ile Leu Thr His Thr Ile Ser Val Pro
 100 105 110

Tyr Val Thr Asp Thr Val Leu Pro Ile Leu Ile Glu His Ser Pro Gln
 115 120 125

Ala Val Trp Leu Phe Ala Asn Asp Pro Asp Phe Glu Ala Ser Ser Glu
 130 135 140

Pro Gly Ala Lys Gly Thr Ala Lys Gln Ile Ile Glu Ala Leu His Ala
 145 150 155 160

Ser Gly Phe Val Val Phe Phe Gln Val Gly Thr Val Lys Asp Ala Arg
 165 170 175

Lys Ala Ala Ala Asp Gly Ala Asp Val Ile Val Ala Gln Gly Ile Asp
 180 185 190

Ala Gly Gly His Gln Leu Ala Thr Gly Ser Gly Ile Val Ser Leu Val
 195 200 205

Pro Glu Val Arg Asp Met Leu Asp Arg Glu Phe Lys Glu Arg Glu Val
 210 215 220

Val Val Val Ala Ala Gly Gly Val Ala Asp Gly Arg Gly Val Val Gly
 225 230 235 240

Ala Leu Gly Leu Gly Ala Glu Gly Val Val Leu Gly Thr Arg Phe Thr
 245 250 255

Val Ala Val Glu Ala Ser Thr Pro Glu Phe Arg Arg Lys Val Ile Leu
 260 265 270

Glu Thr Asn Asp Gly Gly Leu Asn Thr Val Lys Ser His Phe His Asp
 275 280 285

Gln Ile Asn Cys Asn Thr Ile Trp His Asn Val Tyr Asp Gly Arg Ala

290

295

300

Val Arg Asn Ala Ser Tyr Asp Asp His Ala Ala Gly Val Pro Phe Glu
 305 310 315 320

Glu Asn His Lys Lys Phe Lys Glu Ala Ala Ser Ser Gly Asp Asn Ser
 325 330 335

Arg Ala Val Thr Trp Ser Gly Thr Ala Val Gly Leu Ile Lys Asp Gln
 340 345 350

Arg Pro Ala Gly Asp Ile Val Arg Glu Leu Arg Glu Glu Ala Lys Glu
 355 360 365

Arg Ile Lys Lys Ile Gln Ala Phe Ala Ala
 370 375

<210> 45

<211> 195

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabK Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=Ile or Ala

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> X=Gly or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X=Gly or Pro

<220>

<221> MISC_FEATURE

<222> (8)..(16)

<223> X=any amino acid and up to 3 may be absent

<220>
<221> MISC_FEATURE
<222> (18)..(19)
<223> X=Pro, Ala, Gly, Ser or Thr

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> X=Ser or Ala

<220>
<221> MISC_FEATURE
<222> (22)..(23)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (26)..(53)
<223> X=any amino acid and up to 6 may be absent

<220>
<221> MISC_FEATURE
<222> (55)..(55)
<223> X=Gln, Asn, Glu or Asp

<220>
<221> MISC_FEATURE
<222> (56)..(56)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (59)..(59)
<223> X=Gly or Ala

<220>
<221> MISC_FEATURE
<222> (61)..(165)
<223> X=any amino acid and up to 15 may be absent

<220>
<221> MISC_FEATURE
<222> (167)..(168)
<223> X=Ile or Val

<220>
<221> MISC_FEATURE
<222> (169)..(169)
<223> X=Ala or Gly

<220>

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 145 150 155 160

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa
 165 170 175

Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Leu Gly Ala Xaa Xaa Xaa Xaa Xaa
 180 185 190

Gly Thr Arg
 195

<210> 46
 <211> 60
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: A FabK Consensus Sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X=Ile or Val

<220>
 <221> MISC_FEATURE
 <222> (3)..(4)
 <223> X=any amino acid

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X=Gly or Ala

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> X=Gly or Pro

<220>

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val
50 55 60

<210> 47
<211> 1167
<212> DNA
<213> Staphylococcus aureus NCTC 8325

<400> 47
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actcaaatgt taagtattga atatccaatt attacagcag gtttggcagg aagtacgacc 180
cccaaattag ttgcattaat taataacagt ggtggggttag gcacaatagg cgaggttac 240
tttaatacgc agcaattgga agatgaaata gattatgtac gccaatbaac gtcaaattct 300
tttggcgtaa atgtctttgt accaagtcaa caatcatata ccagtagtca aattgaaaat 360
atgaatgcat gggtaaaacc ttatcgacgc gcattacatt tagaagagcc ggttgtaaaa 420
attaccgaag aacaacaatt taagtgtcat attgatacga taattaaaaa gcaagtgcct 480
gtatgttggt ttacttttgg aattccaagc gaacagatta taagcagggt gaaagcagcg 540
aatgtcaaac ttataggtac agcaacaagt gttgatgaag ctattgcaa tgaaaaagcg 600
ggtaggtatg ctatcgttgc tcaaggtagt gaagcagggtg gacatcgtgg ttcatTTTTA 660
aaacctaata atcaattacc tatggttggg acaatatctt tagtgccaca aattgtagat 720
gtcgtttcaa ttccgggtcat tgccgctggt ggaattatgg atggtagagg agttttggca 780
agtattgtct taggtgcaga aggggtacaa atgggcaccg catttttaac atcacaagac 840
agtaatgcat cagaactact gcgagatgca attataaata gtaaagaaac agatacagtc 900
attacaaaag cgtttagtgg aaagcttgca cgcggtatca acaatagggt tatcgaagaa 960
atgtcccaat acgaaggcga tatccagat tatccaatac aaaatgagct aacaagtagc 1020
ataagaaaag ccgcagcaaa catcggcgac aaagagttaa tacatatgtg gagtggacaa 1080
agcccgcgac tagcaacaac gcatcccgcc aacaccatca tgtccaatat aatcaatcaa 1140
attaatcaaa tcatgcaata taaataa 1167

<210> 48
<211> 355
<212> PRT
<213> Staphylococcus aureus NCTC 8325

<400> 48

Met Trp Asn Lys Asn Arg Leu Thr Gln Met Leu Ser Ile Glu Tyr Pro
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Ile Ile Thr Ala Gly Leu Ala Gly Ser Thr Thr Pro Lys Leu Val Ala
 20 25 30

Leu Ile Asn Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
 35 40 45

Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
 50 55 60

Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
 65 70 75 80

Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
 85 90 95

Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
 100 105 110

Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
 245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
340 345 350

Gln Tyr Lys
355

<210> 49

<211> 753

<212> DNA

<213> FabI Bacillus subtilis

<400> 49

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atggaacaaa ataaatgtgc actcgtaaca ggaagcagcc gcggtgtcgg aaaagcggcc      60
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gcagcattag aaacagcggg agaaatcgaa aagcttggcg ttaaagtgct tgtcgtaaaa      180
gcaaacgtag gacagcctgc aaaaatcaaa gaaatgtttc agcaaattga tgaaacgttc      240
ggcagacttg atgtttttgt caataatgcc gottcaggag tactaagacc tgtcatggaa      300
ttagaagaaa cacactggga ctggacgatg aacattaatg cgaaagcatt gcttttctgc      360
gctcaggaag ctgccaaagt aatggagaag aacggtggcg ggcattattgt cagcattagt      420
tcattaggct ctatccgcta tcttgaaaac tacaccacgg tcggtgtatc aaaagcagcg      480
ttagaggctt taaccggtta tcttgccggt gagctttcac caaaacaaat tatcgtcaat      540
gctgtttcag gcggagcgat cgacacagat gcgctgaagc acttcccgaa tagagaagat      600
ctgcttgagg atgcgcgcca aaatacgccg gcgggacgca tggtcgaaat taaagacatg      660
gttgatactg tggagtttct agtgtcttcc aaggctgaca tgatccgcgg acagacaatt      720
atcgttgacg gcggacgctc actgctcggt taa                                     753

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<210> 50
 <211> 250
 <212> PRT
 <213> FabI Bacillus subtilis

<400> 50

Met Glu Gln Asn Lys Cys Ala Leu Val Thr Gly Ser Ser Arg Gly Val
 1 5 10 15

Gly Lys Ala Ala Ala Ile Arg Leu Ala Glu Asn Gly Tyr Asn Ile Val
 20 25 30

Ile Asn Tyr Ala Arg Ser Lys Lys Ala Ala Leu Glu Thr Ala Glu Glu
 35 40 45

Ile Glu Lys Leu Gly Val Lys Val Leu Val Val Lys Ala Asn Val Gly
 50 55 60

Gln Pro Ala Lys Ile Lys Glu Met Phe Gln Gln Ile Asp Glu Thr Phe
 65 70 75 80

Gly Arg Leu Asp Val Phe Val Asn Asn Ala Ala Ser Gly Val Leu Arg
 85 90 95

Pro Val Met Glu Leu Glu Glu Thr His Trp Asp Trp Thr Met Asn Ile
 100 105 110

Asn Ala Lys Ala Leu Leu Phe Cys Ala Gln Glu Ala Ala Lys Leu Met
 115 120 125

Glu Lys Asn Gly Gly Gly His Ile Val Ser Ile Ser Ser Leu Gly Ser
 130 135 140

Ile Arg Tyr Leu Glu Asn Tyr Thr Thr Val Gly Val Ser Lys Ala Ala
 145 150 155 160

Leu Glu Ala Leu Thr Arg Tyr Leu Ala Val Glu Leu Ser Pro Lys Gln
 165 170 175

Ile Ile Val Asn Ala Val Ser Gly Gly Ala Ile Asp Thr Asp Ala Leu
 180 185 190

Lys His Phe Pro Asn Arg Glu Asp Leu Leu Glu Asp Ala Arg Gln Asn
 195 200 205

Thr Pro Ala Gly Arg Met Val Glu Ile Lys Asp Met Val Asp Thr Val
 210 215 220

Asn Ile Ala Phe Thr Tyr Asn Ser Asn Ala Gln Ile Ala Asp Glu Met
35 40 45

Val Gln Asp Leu Glu Lys Asn Tyr Lys Ile Lys Ala Arg Ala Tyr Glu
 50 55 60
 Phe Asn Ile Leu Glu Pro Glu Thr Tyr Lys Glu Leu Phe Glu Lys Ile
 65 70 75 80
 Asp Val Asp Phe Asp Arg Val Asp Tyr Phe Ile Ser Asn Ala Ile Ile
 85 90 95
 Ser Gly Arg Ala Val Val Gly Gly Tyr Thr Lys Phe Met Lys Leu Lys
 100 105 110
 Pro Lys Gly Ile Asn Asn Ile Phe Thr Ala Thr Val Asn Ala Phe Val
 115 120 125
 Val Gly Ala Gln Glu Ala Ala Lys Arg Met Glu Lys Val Gly Gly Gly
 130 135 140
 Ser Ile Ile Ser Ile Ser Ser Thr Gly Asn Leu Val Tyr Ile Glu Asn
 145 150 155 160
 Tyr Ser Gly His Gly Thr Ala Lys Ala Ala Val Glu Ala Met Ala Arg
 165 170 175
 Tyr Ala Ala Thr Glu Leu Gly Glu Lys Asn Ile Arg Val Asn Val Val
 180 185 190
 Ser Gly Gly Pro Ile Lys Thr Asp Ala Leu Arg Ala Phe Thr Asn Tyr
 195 200 205
 Glu Glu Val Lys Gln Ala Thr Ile Asn Leu Ser Pro Leu Asn Arg Met
 210 215 220
 Gly Gln Pro Glu Asp Leu Ala Gly Ala Cys Leu Phe Leu Cys Ser Ser
 225 230 235 240
 Lys Ala Ser Trp Val Thr Gly His Thr Phe Ile Val Asp Gly Gly Thr
 245 250 255
 Thr Phe Lys

<210> 53
 <211> 789
 <212> DNA
 <213> Helicobacter pylori FabI

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<400> 53
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aataaaaaatg ttgaagaagc caacaaaatc atagaagatg tggagcaaaa atattccatt 180
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caaattgacg ctgattttga cagagtggat ttttttattt ctaacgctat tatttatggg 300
cgttctgtcg tgggggggatt tgcaccgttt atgcgattaa aacctaaggg gttaaacaac 360
atttacacag ccaccgtggt agcgttcgct gtaggggctc aagaagcggc aaaacgcatg 420
caaaaaatag gcggtggggc gatcgtgagc ttaagttcta ccgggaatct agtttatatg 480
cctaattacg ccgggcatgg caattccaaa aacgccgtag aaaccatggt caaatagcgt 540
gccgtggatt taggcgaatt taacattaga gtgaatgcgg ttagtggcgg gcctattgat 600
acggacgctt tgaaagcctt ccctgattat gtggagatta aagaaaaagt agaagagcaa 660
tcgcccctaa aacgcatggg caatcctaac gatctagccg gagcggctta ttttttatgc 720
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<210> 54
<211> 262
<212> PRT
<213> Helicobacter pylori FabI

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<400> 54

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Met Asn Gly Ser Asn His Met Lys Asn Lys Thr Leu Val Ile Ser Gly
1          5          10          15

```

```

Ala Thr Arg Gly Ile Gly Lys Ala Ile Phe Val Arg Phe Ala Gln Ser
20          25          30

```

```

Gly Val Asn Ile Ala Phe Thr Tyr Asn Lys Asn Val Glu Glu Ala Asn
35          40          45

```

```

Lys Ile Ile Glu Asp Val Glu Gln Lys Tyr Ser Ile Lys Ala Lys Ala
50          55          60

```

```

Tyr Ser Leu Asn Val Leu Glu Pro Glu Gln Tyr Thr Glu Leu Phe Lys
65          70          75          80

```

```

Gln Ile Asp Ala Asp Phe Asp Arg Val Asp Phe Phe Ile Ser Asn Ala
85          90          95

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Ile Ile Tyr Gly Arg Ser Val Val Gly Gly Phe Ala Pro Phe Met Arg
 100 105 110

Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val Leu Ala
 115 120 125

Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys Ile Gly
 130 135 140

Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val Tyr Met
 145 150 155 160

Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu Thr Met
 165 170 175

Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg Val Asn
 180 185 190

Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala Phe Pro
 195 200 205

Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro Leu Lys
 210 215 220

Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe Leu Cys
 225 230 235 240

Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val Val Asp
 245 250 255

Gly Gly Thr Thr Phe Lys
 260

<210> 55

<211> 843

<212> DNA

<213> FabI Streptomyces collinus

<400> 55

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gtcgtcaact acaagaagaa cgccgacctg gcacagaaga ccgtcgccga ggctcaggag 180

gccggtggcc agggcttcgc ggtccaggcg gacgtcgaga ccaccgaggg ggctcaggcg 240

ctgttcgacg aggtggcgca gcgctcgggg aggtcgcgc acttcgtctc caacgcggcg 300

gcgagcgcgt tcaagaacat cgtcgatctc ggccccgacc acctggaccg ctcgtagcgc 360
 atgaacctgc ggcccttcgt gctgggggcg caacaggccg tgaagctgat ggacaacggc 420
 ggacggatcg tcgcgtgtc ctctacggc tcgggtccgc cctaccccac ctacgcgatg 480
 ctcgggcgga tgaaagccgc catcgagtca tgggtgcggt acatggcggg ggagttcgct 540
 ccttacggca tcaacgtcaa cgcgggtcaac ggcgccctga tcgactccga ttcgctggag 600
 ttctttctaca acgtcgaggg catgcgcgcc atgcaggggc tcctcgaccg catccccgcg 660
 cgccgtccgg gcaccgtaca ggagatggcc gacaccatcg ccttcctgct cggcgacgga 720
 gcgggttaca tcaccgggca gaccctcgtg gtcgacggcg ggctcagcat cgtcgcgccg 780
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 tga 843

<210> 56
 <211> 280
 <212> PRT
 <213> FabI Streptomyces collinus

<400> 56

Met Asn Ser Pro His Gln Gln Gln Thr Ala Asp Arg Arg Gln Val Ser
1 5 10 15

Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Arg Thr Leu Ala Leu Thr
20 25 30

Leu Ala Arg Arg Gly Gly Thr Val Val Val Asn Tyr Lys Lys Asn Ala
35 40 45

Asp Leu Ala Gln Lys Thr Val Ala Glu Val Glu Glu Ala Gly Gly Gln
50 55 60

Gly Phe Ala Val Gln Ala Asp Val Glu Thr Thr Glu Gly Val Thr Ala
65 70 75 80

Leu Phe Asp Glu Val Ala Gln Arg Cys Gly Arg Leu Asp His Phe Val
85 90 95

Ser Asn Ala Ala Ala Ser Ala Phe Lys Asn Ile Val Asp Leu Gly Pro
100 105 110

His His Leu Asp Arg Ser Tyr Ala Met Asn Leu Arg Pro Phe Val Leu
115 120 125

Gly Ala Gln Gln Ala Val Lys Leu Met Asp Asn Gly Gly Arg Ile Val

130		135		140
Ala Leu Ser Ser Tyr Gly Ser Val Arg Ala Tyr Pro Thr Tyr Ala Met				
145		150		155 160
Leu Gly Gly Met Lys Ala Ala Ile Glu Ser Trp Val Arg Tyr Met Ala				
	165		170	175
Val Glu Phe Ala Pro Tyr Gly Ile Asn Val Asn Ala Val Asn Gly Gly				
	180		185	190
Leu Ile Asp Ser Asp Ser Leu Glu Phe Phe Tyr Asn Val Glu Gly Met				
	195		200	205
Pro Pro Met Gln Gly Val Leu Asp Arg Ile Pro Ala Arg Arg Pro Gly				
	210		215	220
Thr Val Gln Glu Met Ala Asp Thr Ile Ala Phe Leu Leu Gly Asp Gly				
	225		230	235 240
Ala Gly Tyr Ile Thr Gly Gln Thr Leu Val Val Asp Gly Gly Leu Ser				
	245		250	255
Ile Val Ala Pro Pro Phe Phe Ala Asp Ala Gly Glu Ala Leu Glu Leu				
	260		265	270
Pro Pro Arg Pro Thr Arg Asp Ala				
	275		280	

<210> 57
 <211> 176
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: A FabI Consensus Sequence

<220>
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 <222> (2)..(2)
 <223> X=Ala, Gly, Ser, Pro, or Thr

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X=Pro, Ala, Gly, Thr, or Ser

<220>
 <221> MISC_FEATURE

<222> (6)..(6)
<223> X=Ile, Val, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (8)..(127)
<223> X=any amino acid and up to 20 may be absent

<220>
<221> MISC_FEATURE
<222> (130)..(130)
<223> X=Glu, Gln, Asn, or Asp

<220>
<221> MISC_FEATURE
<222> (132)..(132)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (134)..(134)
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<220>
<221> MISC_FEATURE
<222> (136)..(159)
<223> X=any amino acid and up to 6 may be absent

<220>
<221> MISC_FEATURE
<222> (161)..(166)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (168)..(168)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (170)..(170)
<223> X=Val, Ile, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (172)..(172)
<223> X=Thr, Ala, Ser, Pro, or Gly

<220>
<221> MISC_FEATURE
<222> (173)..(174)

<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (175)..(175)

<223> X=Lys, Arg, or His

<400> 57

Gly Xaa Xaa Arg Gly Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
115 120 125

Gln Xaa Ala Xaa Lys Xaa Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Tyr
165 170 175

<210> 58

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabI Consensus Sequence

<220>

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<222> (2)..(2)

<223> X=Ala, Gly, Ser, Pro, or Thr

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<221> MISC_FEATURE

<222> (3)..(3)

<223> X=Pro, Ala, Gly, Thr, or Ser

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<221> MISC_FEATURE

<222> (6)..(6)

<223> X=Ile, Val, Leu, or Met

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> X=any amino acid

<400> 58

Gly Xaa Xaa Arg Gly Xaa Gly Xaa
1 5

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 59

tctagacata tgaaaacgcg tattacagaa tta

33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 60

ggatcctaga tactgggcac cttgacc

27

<210> 61

<211> 5

<212> PRT

<213> Unknown

<220>
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<221> MISC_FEATURE
<222> (2)..(4)
<223> X=any amino acid

<400> 61

Tyr Xaa Xaa Xaa Lys
1 5

<210> 62
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: A Enoyl Reductase Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (2)..(7)
<223> X=any amino acid

<400> 62

Thr Xaa Xaa Xaa Xaa Xaa Lys
1 5